

**FIGURE 8**

GCCCCGCGCCCGGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCGCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCGCAGCCGCAACTCCACCGTGAGCCGCGCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTTGGGTCTCTTCTCTTCA  
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCGATTCCCGTGCTGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTCTATGATGACGCTCACCAACTGGTACAAGCCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCGAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTTCCCCTCCTCCTGT  
TGCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

**FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SOLYKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSW  
NQRWLGAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFIISLNLTFC  
VCVSIAAVLPKVQDAQPNISGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQA  
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

**FIGURE 10**

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG  
TGACTGCCGATTCCGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTGCTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTGAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

**FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318  
><subunit 1 of 1, 285 aa, 1 stop  
><MW: 32190, pI: 9.03, NX(S/T): 2  
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEIYHNRFDAVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLEFRINVGLR  
GLVAGGIIGALLGTFVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

**Important Features:****Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and amino acids 171-195

**N-glycosylation site:**

amino acids 153-156

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**FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG  
GCTGGCGCCGAACC

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGTGCGGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

[illegible]

**FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979  
><subunit 1 of 1, 204 aa, 1 stop  
><MW: 22147, pI: 8.37, NX(S/T): 3  
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACALNQEQQGQQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

**Signal Peptide:**

amino acids 1-34

**Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

**FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCACTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCGGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCTTGC

**FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

**FIGURE 19**

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTGACACAAAGTTGCCCCTGCAGAGGTGAGCTGCCCGC  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA  
GGAGGCCCTGGGCCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCCAGTGTTTTGTGTTAGAATAATGTAGTTAGGTGAGTGAAATAAATT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCACAAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCCGCAACACCG  
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAATTCTGG  
TTGTTTGTAGCCTAA



**FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594  
><subunit 1 of 1, 359 aa, 1 stop  
><MW: 38899, pI: 5.21, NX(S/T): 0  
MKLGCVLMAWALYLSLGVLVVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

**FIGURE 21**

CCCACGCGTCCGCCCCACGCGTCCGCCCCACGGGTCCGCCCCACGCGTCCGGGCCACCAGAAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGAGGCCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAAATTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACTTCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCCCAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

**FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416  
><subunit 1 of 1, 321 aa, 1 stop  
><MW: 35544, pI: 8.51, NX(S/T): 0  
MGILLGLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKQVVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 276-306

## FIGURE 23

GGCGCCGGGAGCCCATCTGCCCCCAGGGGCGACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCCGAGGTCCGTCCGA  
GGCGCCCGGCGCGCCCGGAGCCCAAGCAGCAACTCAGCGGGGAAGCGCCCGCGTCCGCGGATC  
GGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCAGCTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
CCAGTGATCAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAAGTGTACAGT  
ATGTACAAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCAACACCCAGCATGATCCCCAGCCAGAGCAGACCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTCTCCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTCTTCTTATACAATACCAAACAAGCAAA  
AGGATGTAAGCTGATTGATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAAACTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCCTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTGATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAAT  
CAGATGCCTCTAAGGACTTCTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCATT  
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV
```

Transmembrane domain:

amino acids 221-254

**FIGURE 25**

GTCTGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGAG  
GAGAGCACCCGGAGACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCCTCGCC  
GCTGGGCAGGTGCTGAGCGCCCTAGAGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGGCCGC  
AGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGGCCGGGAGGCGGCGGTGGATGC  
GGCGCTGGGCAGAAAGCAGCCGCGGATTCCAGCTGCCCCGCGCGCCCCGGGCGCCCCCTGCGAG  
TCCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGC  
ATCGCCCCGGGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTTAG  
CACCACCACAGCTCAGCCAGAACAGAAGGCCTCGAATCTCATTGGCACATAACGCCATGTTG  
ACCGTGCCACCGGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTCTCTGAG  
CATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGGGGACCTTTACCAGGCA  
TGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGATTGAGA  
AATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACCTGCCACCTGGCATGTTCCAGTCT  
AACGCTACCTGTGCCCCCCTACGGTGTGTCTGTGGGTTGGGGTGTGCGGAAGAAAGGGAC  
AGAGACTGAGGATGTGCGGTGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTA  
GTGTGATGAAATGCAAAGCATAACAGACTGTCTGAGTCAGAACCTGGTGGTGTCAAGCCG  
GGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTCTCCAGCTCCACCTCACC  
TTCCTTGGCACAGCCATCTTTCCACGCCCCGAGCACATGGAAACCCATGAAGTCCCTTCT  
CCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCA  
AAGGTACTGATAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAA  
GGAAGACGTGAACAAGACCCCTCCCAAACCTTCAGGTAGTCAACCACAGCAAGGCCCCCACC  
ACAGACACATCCTGAAGCTGCTGCCGTCCATGGAGGCCACTGGGGGCGAGAAGTCCAGACG  
CCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAGCATTTTGACATCAA  
TGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGTGGTGTGTTGTGGTGT  
GCAGTATCCGGAAGAGCTCGAGGACTCTGAAAAGGGGGCCCCGGCAGGATCCCAGTGCCATT  
GTGGAAGAGGAGGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTA  
CTACTGCAATGGCCATGGTATCGATATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGT  
GGAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAGAGGGAGGTTGCTGCTTTCTCCAAT  
GGGTACACAGCCGACCAGGCGGGCCTCACAGCTCTGCAGCACTGGACCATCCGGGGCCCC  
CGAGGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGG  
AGAAGATTCTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCG  
ATGAGCCCCAGCCCGCTTAGCCCCAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTC  
CGCTCTCCTGACGGTGGAGCCTTCCCCACAGGACAAGAACAAGGGCTTCTCGTGGATGAGT  
CGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCCTCCGCGCTGAGCAGGAACGGT  
TCCTTTATTACCAAAGAAAAGAGACACAGTGTGCGGCAGGTACGCCTGGACCCCTGTGA  
CTTGACGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTG  
AAGAGATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGC  
CAGGAAGCCAGCCAGACCCCTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAA  
CATAGGGATACTGCATTCTGGAAATTACTCAATTTAGTGGCAGGGTGGTTTTTTAATTTTCT  
TCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
GTGTGTGTGTGTGTGTTAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCCTTCTCTCTCT  
CTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAC  
GTTGTGAAATACCCACCCTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTA  
TGTATTTTCAAGATTATTCTGTGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGA  
CTTTTCCACACACTGGATTGTGAGGCTCTTAACTTCTTAAAAGTATAATGGCATCTTGTGA  
ATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTTTAAAAACAAATATTAT  
TACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGACC  
CCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTT  
CATATTGAGCTGAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCG  
TGTAAGTCTGATTACTTGTACTCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAA  
ATCCTCAAGCCATCAGGATTTGCTATTTAGTGGCTTGACAACCTGGGCCACCAAAGAACTTG  
AACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTTGGAAAGTCAAAA  
TCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAAGATGTCTT  
GTTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGA  
TTCCTTCACCAATTACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGTCTGATATAT  
TTGCAACTATGCTCCCATTTACAAATGTACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCA  
AAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGGGTAGTGGTGAAGGACCGATATC  
AGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTAAAAA

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGLFSTTTAQPEQKASNLIQTYRHVD RATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLP CA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTTETEDVRCCKQCARGTFSDVPSSVMKC
KAYTDCLSQLVVIKPGTKETDNVCGTLPFSSTSPSPGTAIFRPREHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPLNLQVVNHQOGPHRRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPQTQNRKWIYYCNGHGIDILKLVA AQVGSQWKDIY
QFLCNASEREVA AFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALS RNGSFITKEKKD TVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDR LFEIIGVKSQEASOTLLDSVYSHLPDLL
```

**FIGURE 27**

ATGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTCGAAATAGTCAC  
CATCGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCGGATCGCTTTTGGCC  
TTGATGATTTGAAAATAAGTCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCTGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGGTGGGTGGTCAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC  
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTC  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT  
GTGGTCATAGAAGGGGCTACAGCTCAGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCTCATC  
GCCCCGTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGA  
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCAGGTGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTCACTCTCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGAGCTCTGAGTTCCGGCACCA  
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT  
GTTTTTTGTTTTTTTGAAGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA  
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTTAGTAGAGAC  
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
CAGCCTCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCAGCTCCTTTT  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG  
TGCAAGGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC  
ACTGCACGTTTTCTCTAGGGACCAGAACCAACCCACCCTTTCTACTTCCAAGACTTAT  
TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCTTCCCT  
CATGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA



**FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV TALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAACHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSF GIGCAEVNKP G VYT
RVTSFLDWIHEQMERDLKT
```

**FIGURE 29**

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTC  
AAGGCTGGCTTGTGCCAGAACGGCGCGCGCGCGCACGCACACACACGGGGGAAAC  
TTTTTTAAAAATGAAAGGCTAGAAGAGCTCAGCGGCGGGCGGGCGCTGCGCGAGGGCTCCG  
GAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTGCAGACGCCCGGCCCGGCTCGGCCCC  
GCGTGGGATGGTGCAGCGCTCGCCGCGGGCCCCGAGAGCTGCTGCACTGAAGGCCGGGACG  
**ATGG**CAGCGCGCCCGCTGCCCGTGTCCCCCGCCGCGCCCTCCTGCTCGCCCTGGCCGGTGC  
TCTGCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAG  
TTGTCACTGCCTCTGTTCCGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAG  
AATCATCCAGAAGTGCTGAATATTCGACTACAACGGGAAAGCAAAGAAGTATCATAAATCT  
GGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAACCCACTATCTGCAAGACGGTA  
CTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGTACGGGGA  
TATTCTGATTGACAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGA  
AAATGAAAGCTATGTCTTAGAACCAATGAAAGTGCAACCAACAGATACAAACTCTTCCCAG  
CGAAGAAGCTGAAAAGCGTCCGGGGATCATGTGGATCACATCACAAACACACCAACCTCGCT  
GCAAAGAATGTGTTTCCACCACCCTCTCAGACATGGGCAAGAAGGCATAAAAGAGAGACCCT  
CAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCGAGAGTTTCAGAGGCAAG  
GAAAAGATCTGGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAAGTTT  
TACAGACCACTGAACATTCCGGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAA  
ATGCTCTGTAAGTCAGGACCCATTACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGA  
AGCTTCTACCTCGCAAATCCCATGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAAGGG  
ACCACCATCGGCATGGCCCAATCATGAGCATGTGCACGGCAGACCACTCTGGGGGAATTGT  
CATGGACCATTGACACAATCCCCTTGGTGCAGCCGTGACCCTGGCACATGAGCTGGGCCACA  
ATTTCCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAAA  
GGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAG  
CAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCCG  
AAGTCAGGGAGTCTTTCGGGGGCCAGAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAG  
TGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTGCTGCAATGCCACCACCTGTACCCT  
GAAGCCGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCTGAAGCCTGCAG  
GAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGC  
CCTCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTA  
CTGCTACAATGGCATCTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTG  
CTAAACCTGCCCCTGGGATCTGCTTTGAGAGAGTCAATTCTGCAGGTGATCCTTATGGCAAC  
TGTGGCAAAGTCTCGAAGAGTTCTTTTGCCAAATGCGAGATGAGAGATGCTAAATGTGGAAA  
AATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTCCATAGAAA  
CAAACCTCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCAGTGTACTTGGGC  
GATGACATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGAAAAATCTG  
CCTGAATCGTCAATGTCAAAATATTAGTGTCTTTGGGGTTACAGAGTGTGCAATGCAGTGCC  
ACGGCAGAGGGGTGTGCAACAACAGGAAGAACTGCCACTGCGAGGCCCACTGGGCACCTCCC  
TTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCCATCCGGCAAGCAGAAGC  
AAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGGATCGC  
AGGAGCATGCGTCTACTGCCTCACTGACACTCATCT**GAG**CCCTCCCATGACATGGAGACCGT  
GACCAGTGGCTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGA  
CTCTGTGGCTTTGCCATCGTTTTCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAG  
GGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAACAGTGCAAGGAAGGGCAGCGACTTCCTG  
GTTGAGCTTCTGCTAAAAATGACATGCTTCAGTGTGCTCCTGAGAGAGTAGCAGGTTAC  
CACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTAC  
TGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGTTGGGGCCAGTGTCCCCTTTCCCCAGTGA  
CACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGC  
TTTTAGCATTTATTATATGAAAATAGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCC  
ACCCATTCCATCTCCATCCAAGCAAAGTGAATGGCAATGAAACAACTGGAGAAGAAGGTAG  
GAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGCAGTCAAGTT  
TGAGGGTTTGCAGAAAGCCAGGGAAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGA  
ATGTTAAAAAGTGAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAA  
AATAGAGTGCATTTGAAAT

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624  
><subunit 1 of 1, 735 aa, 1 stop  
><MW: 80177, pI: 7.08, NX(S/T): 5  
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK  
YRPLNIRIVLVGVEVWMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVSKESSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLGATKCADGKICLNRCQNI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGQGQEPVGSQEHASTASLTLI

**FIGURE 31**

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

[illegible]

**FIGURE 33**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL

LHLYH

FIGURE 34

CCGCGCGCGAGAGCGCGCCACGCCCGCCGCGCATGCCCGCGCGCCACGACGACCTCCTCCCG  
CTGCTGGCCCGCGCGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGG  
CGGGCGCTGGGGCGCCCGGGCCAGGAGGCGGCGGCGGCGGCGGACGGGCCCCCGCGG  
CAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACCTGTACACGGCCGACATGTTACAG  
CACGGGATCCAGAGCGCCGCGCACTTCGTATGTTCTTCGCGCCCTGGTGTGGACACTGCCA  
GCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAG  
TCTATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAGGGGGTGC  
GGATACCCACCTTAAAGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCG  
GGACTCCAGACACTGGAAACTGGATGCTGCAGACACTGAACGAGGAGCCAGTGACACCAG  
AGCCGGAAGTGAACCGCCAGTGCCCGGAGCTCAAGCAAGGGCTGTATGAGCTCTCAGCA  
AGCAACTTTGAGCTGCAGTTGCACAGGCGACCACCTTTATCAAGTCTCTCGCTCCGTGGTG  
TGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGTGGCTTGGGCCCTTGAACATTCGG  
AACTGTCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAACCCAG  
GTTCTGGCTATCCCACTCTTCTCTGGTTCGAGATGGGAAAAAGGTGGATCAGTACAAGGG  
AAAGCGGGATTTGGAGTCACTGAGGGAGTACGTGGAGTCGCAGCTGCAGCGCACAGAGACTG  
GAGCGACGGAGACCGTACGCCCCCTCAGAGGCCCGGTGCTGGCAGCTGAGCCCAGGGCTGAC  
AAGGGCACTGTGTTGGCACTCACTGAAAAATAACTTCGATGACACCATTGCAGAAGGAATAAC  
CTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGG  
AACTCTCTAAAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACT  
GCTGAACGGAATATCTGCAGCAAGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCG  
AGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCAGAGACCTTGACTCGTTACACCGCTTG  
TCCTGAGCCAAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTACCTCTCCTGCCACG  
TCCCGCACCTCGCTTTAGGAGTTCACTCCACAGAGGCCAGCTGGGTCCCAGTGGTGGCTG  
TTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTTTCCAGGCCAA  
CACACTCTACAGATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCAC  
TGTGTAAACATTTTTCAGTGGCGATATATCCCTTTGACCTTCTCTTGATGAAATTTACATGG  
TTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAATTGCTGGACTATTTGTGGCTCCTG  
AGTTGAGTGATTTTGGTGAAGAAAGCACATCCAAAGCATAGTTTACCTGCCACGAGTTCT  
GGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAAT  
ACTGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATAC  
CTTCACGGCCGCTGCTGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGC  
CGTGATGAAAGCAGCGTTACTTCTGACCGTGCTGAGTAAGAGAATGCTGATGCCATAACTT  
TATGTGTCGATACTTGTCAAATCAGTTACTGTTTCAAGGGATCCTTCTGTTTTCTACGGGGTG  
AAACATGTCTTTAGTTCTCTATGTTTAAACAGAACCCAGAGCCACATGAACCTGTTGGATGTC  
TTCTTAGAAAGGGTAGGCATGGAATACTCCACGAGGCTCATCTCAGTATCTCATTAACTC  
ATTGAAAGATTCCAGTTGTATTTGTACACTTGGGGTGACAAGACCAGACAGGCTTTCCAGGC  
CTGGGTATCCAGGGAGGCTCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTC  
TGATTCTGTTTCTCAGTAGTCCTTTTAGAGGCTTGCTATACTTGGTCTGCTTCAAGGAGGTG  
GACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGACCAAAGACAGATGTCAGTG  
GGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTAACTCA  
TGCTGTCTTGTGATTAAACACCTCTATCTCCTTGGGAATAAGCACATACAGGCTTAAGCT  
CTAAGATAGATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCA  
TCCAACACTCTTCACCCACCTCCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACT  
GGTGGTAGGAATCTTAGAAACAAGACCACTTATACTGTCTGTCTGAGGCAGAAGATAACAGC  
AGCATCTCGACACCGCTCTGCCTTAAAGGAAATCTTTATTAATCACGTATGGTTCACAGATA  
ATTCTTTTTTTTAAAAAACCCACCTCTGATAGAGACAACTGTCAAGAGTCTTGTACACA  
CAACTTCAGCTTTGCATCACGAGCTTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTT  
GTTTACACTATGATACTTTCTAAATAAACTCTTTTTTTTTTAA

**FIGURE 35**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMQLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFEHVAQGDHFIFKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGGKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDOTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```



**FIGURE 36**

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAAATCCCTAACCCACTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAA

**FIGURE 37**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDGPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGGRY
RKFGVQQLDISIARLKTSMKFVKNIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK
```

**FIGURE 38**

GGTTCTATCGATTCTGAATTCTGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACCAGACGGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTACAGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTTCTGTGGCTCTG  
GTTCCGGCTGGCCAAGGCGGCGCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
CCCTCTGCACTGCCTCCGCGCTGCGCGCGCGCGCTGCTGCTGGCGCCAGAGTTTTCTG  
GAGTCCCTGGAGCCGGACCTGCCCCGCGCTGAGAGCCATGGGGCTCCACCTGTGGGCTGACAG  
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCACGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCAGGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCCGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTTGCTTTACAAGC  
ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCCGTAAGCCA  
GCAGTCCCCATTCTTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG  
GCCCGATTCTCAGGCTCCAGGAGTCTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGATGGCAAATGAGGGCTTCGACCCACGACCCCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
CCGTTGCAGGTGTACTGGGCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCACTTGTATTGTCAG

**FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLINGSRFFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRATFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGFPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQQK  
LLKDVFVRPGDVFFNTGDLVCDQGFRLRFHVRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPYVLDQAVGAYLPLTTARYSALLAGNLRI

**Signal peptide:**

aa 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at aa 136

**CUB domain protein motif**

aa 254-261

**putative AMP-binding domain signature**

aa 332-343

**N-glycosylation sites**

aa 37-40 and 483-486

**FIGURE 40**

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCCGAGCGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTTTTAAACACTTCTTTTCTTCTCTCCTCGTTTTGATTGCACCGTTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGCTTGCCATCCT  
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGG  
CTGGCAGAAAGGGGTGACGCTGGGCAGCGCGAGGAGCGCGCGCTGCCTCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTTACCGAGCTGGATTGTATG  
TTGCACCATGCTCTTCTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
AAGGGATTTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCCTTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
GGAACTGAAGATTAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCAGAGCTCGGGGGCTTCCCCTGTGAGGCCCTGCA  
ACAATACTGTCTCAACGTCTGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTTCAGGCCCTACAATCCTGA  
GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTACCA  
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
CTTCTCTTTCTTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTAAAAAT

**FIGURE 41**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKS LNDMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFS EDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLT CIVLALQRLCR
```

## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCT  
GAGAAAACGCACGCAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCG  
GGCTCCGCGCGGACCGGCCGCGGGGCTAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAG  
CGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGTGGAGGGAGATCAGGAAAACGGCTT  
CTTCCTCACTTCGCCGCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGGAAAGGACTGG  
GGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTAT  
CTGTCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCG  
CAGGACAGACGGCCGATCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCT  
CCCCAACGTCGAGGGCGCTCTGGCCACGAAAAGTTTCTGTCCACTGTGATTCTCAATTCCTT  
GCTTGGTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTAACTTTTTTCTTTTTTTTT  
CCTTGGTGGAAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAATGTGCTGGAGAA  
GAGCGAGCCCTCCTTGTTCCTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAA  
AGTTGTGCGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTC  
ACCGTCTGTTGGGTGCATGTGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGG  
GTCTCACCTGGGACCTGAGTGAATGGCTCCAGGGGCTGTGCGGGGCATCCGCCTCCGCCTT  
CTCCACGCTGTGTCTGTCTGCTGGAAGATGCTAGCAATGGGGGCGCTGGCAGGATTCTGG  
ATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCCTTAGAAGAGGAGGAAGA  
AGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCCAGC  
CCCATCTCATTTTTATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCT  
GAGATTAAAACACCTACTCTTGACAAGCTCGCTGCCGAAGGAGTTAAACTGGGAACTACTA  
TGTCCAGCCTATTTGCACACCATCCAGGAGTCAGTTTATTACTGGAAGTATCAGATACACA  
CCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTACCTCTGGACAATGCC  
ACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAATAATGGCACTT  
GGGTTTTTAACAGAAAAGAATGCATGCCACCAGAAAGAGGATTTGATACCTTTTTTGGTTCCC  
TTTTGGGAAGTGGGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTGTGGCTAT  
GACTTGTATGAAAACGACAATGCTGCCTGGGACTATGACAATGGCATATACTCCACACAGAT  
GTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATAACCCCAAAAGCCTATATTTTTAT  
ATACTGCCTATCAAGCTGTTCACTTCAACCTGCAAGCTCCTGGCAGGTATTTGGAACACTAC  
CGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGC  
AATCAACACGTTGACATTGGCTCTAAGACTTATGGTTTTCTATAACAACAGCAATATCATTT  
ACTCTTCAGATAATGGTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCCTCTCAGAGGTAGC  
AAAGGAACATATTTGGGAAGGAGGGATCCGGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAA  
AAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTGACTGGTACCCCACTCTCATTT  
CACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCTGGGAGACC  
ATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACC  
AAGGCAAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGC  
CATCAGAGTGCAGCACTGGAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCC  
CTCAGTCTTTTCAGCAACCTGGGACCGAACCGGTGGCACAAATGAACGGATCACCTTGTCAACT  
GGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGAGAGGGTGGACCTATCTAA  
CAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAACCTGCAG  
TGCCGGTCAGGTATCCCCCAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGG  
GGACCATGGTATAAAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAA  
GCAAAAGAAAAGCAAAAAAAGAAGAAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAA  
ATTTGGCTCGATAATATCGCTGGCCTAAGCGTCAGGCTTGTTTTTCATGCTGTGCCACTCCAG  
AGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGTCTGCTCAGTGCCAAGGTGCTACTCT  
TGCAAGCCACACTTAGAGAGAGTGGAGATGTTTTATTTCTCTCGCTCCTTTAGAAAACGTGGT  
GAGTCCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAAACACTGCTTTGAATTATAGGA  
GGAGAACAATAACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGA  
TTAAAACCTACCTTTGATAAATTACAGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATA  
TATTTTCTTGGTGAATTTTTGTATGTCTGTACATGACACTTGGGTTTTTTAATTAATTCTA  
TTTTATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTTCTCAGATGTGAACA  
GCTTGACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC  
CACAATGAATGTAACCTATTTTCTAAACACTTTACTAGAAGAACATTTAGTATAAAAAACCT  
AATTTATTTTACAGAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAATGACTTTTAT  
TTTTATTTCTGTCATACCATTAGAAGAAATTTATTTTCAATTTCTTCAAATTATCAAGCACTGT  
AATACTATAAATTAATGTAATACTGTGTGAATTCAGACTATAAAAAACATCATTCAGAAAA  
TTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATATTCCTTACAA

**FIGURE 42B**

ATTACTTGGAATTC AATGTTTGTGCAGAGTTGAGACAAC TTTATTGTTTCTATCATAAACT  
ATTTATGTATCTTAATTATTA AAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTT  
TTCTGATCTAACTTCTAGCTAAAATTGTATCATTGGTCCTAAAAAATAAAAAATCTTTACTAA  
TAGGCAATTGAAGGAATGCTTTGCTAACAACCACAGTAATATAATATGATTTTACAGATAGA  
TGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATAACTAATATTTATATT  
AGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAA  
AGTGGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAAC  
CTTGCTTGGAAACCCCA CATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATG  
AAGTTTATCATGGGTCATCAATGAGCATAGATTGGTGTGGATCCTGTAGACCCTGGTGTGTTT  
CTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTACAGTATACACTTGAAAAGTCA  
CAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGTGGTGGTA  
TGACAGCATAACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTA  
TATCAAACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAAT  
GTATAAAAGAATCTATAATCTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGAT  
TTTAATTTTAAACATTTTATTTCTAGAATATATGGCTCCATTTTATTTTATAGTGTAAGTTG  
TATTTCCATAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAGTCTTAAAAATAAAGGCA  
TATTGTTTATGTTTAAA  
AAA



**FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGHYHGSEIKTPTLDKLAAEGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC  
MPTRRGFDTEFFGSLLGSGDYIYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA  
LKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVFVHSPLLKNKGTVCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

**Important Features:**

**Signal Peptide:**

amino acids 1-37

**Sulfatases signature 1.**

amino acids 120-132

**Sulfatases signature 2.**

amino acids 168-177

**Tyrosine kinase phosphorylation site.**

amino acids 163-169

**N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

**FIGURE 44**

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATCGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTGTTAGCATCGGCACGTCAAGCTT  
GGGGTCTGTCACTATGGAACATAAAGTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGGGACCAACAAAT  
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGTCTTTGCTT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAAGTCTAGGACATGTGCCATGATAA  
ACTGTGAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATGTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAAATGTGACA  
TTGGTTTTCGAAGTGAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAAGAACCCACAGGACTCC  
TACCCCTAAGGTGAAGTTCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAGT  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAAGTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAGACATTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAATTGAGTTGTATCAAGGAAGTGTATGC  
TACCAAAAGCATCATTTTTGAAGCAGAAGCTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTGTTTCAAGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGATATTGCATCATAG  
GACCTCTGGCATTTTAGAAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTTACAACATTTCTA  
GAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATTCTTTGTAATAATAA

**FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE  
ATCEPGCKFGECEVGPNNKCRCFPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPTPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

**Signal peptide:**

amino acids 1-21

**EGF-like domain cysteine pattern signature.**

amino acids 80-91

**Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

**FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGCTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATAATGGTGGTGTGGGTGACTGGAGCCTCGAGTGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGCTGTGCTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGGAATGTCCAGCGTTCTCTGTGC  
ATGGATAACCAGCTTGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

**FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMDTSLDVYRKLIENLYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

**Important Features:****Signal Peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 136-157

**Tyrosine kinase phosphorylation site.**

106-113 and 107-114

**Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

**FIGURE 48**

GCAGCGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCCTGTGCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCTGTG  
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTCTACTGCTGCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTGGGTCTCTGACGCTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCCGCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGCCCTGTGCTGTGCCCTCGAGCCTGACGGA  
CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTTCAAGGGGCGAGCTT  
TCCTGGCCCAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGACAGGACCCCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGGAGGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGACGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG  
CATGAGGTGAGGGGCACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAAATGGCATTACTGCCCTGTCTCTCCCAACCCTGTATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC  
AAAATAAAA

**FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571  
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVVQEPQGKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLRLRLISRPTCNCIYNQLHQHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPPEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPDGERG  
WVLGRARPGAGISSLQTVPTLLGPRACSRLLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP  
GSCANISQPTSC

**Important features:**

**Signal peptide:**

amino acids 1-15

**Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

**N-glycosylation sites.**

amino acids 37-40 and 564-567

**Kringle domains**

amino acids 79-96, 343-360 and 235-247

**FIGURE 50**

CGGGCCGCCCCCGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTGAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
GCAGGGCTTGTGTTGATGTGCACAGCGTCTGCGGGTGGTGCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCGCAACCCCGTGTGTCAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTTC  
CCCTCCTTCCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA



**FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386  
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown  
><MW: -1, pI: 4.62, NX(S/T): 4  
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGELEGSKTALQPLKHSDSKED  
DGQEIA

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

**FIGURE 52**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCCTGCG  
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATCCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTTATTTTTATACAATGTTCTTCTTGCTTTGTTTTTTATTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

**FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 24172, pI: 5.99, NX(S/T): 1  
MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 54**

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCCACCCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCTCCAGTTCGCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGGGGGGCTTCTGGCTGTGGTCATCTTGGTGCTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCCACTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTACCTGCCAGTGCTTGCCCTGGCAGTGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGA  
AACTTGAGGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTACGCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAAA

**FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

**FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTGCGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCCC

**FIGURE 57**

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCCCTCCAGTTCCTCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAAGTACGATGTGTGCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

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**FIGURE 58**

TGCGGGGACCGTCGTACACCATGGGGCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCG  
GATGGCCCTCCTGTTCCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGG  
ACGTCAACCCCCAGTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGG  
ACAAGCCGACAGTGCTGCTGCTGCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCTGG  
CTGAACCTGGAAGTGTGCTGCTGCTGCTCATCTGACTGCTGGATTGACAATATCAGGCTGGT  
TTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCT  
TTGGGAAGACCTTCTCACTGGAGTTCCCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTT  
CACACCATGGTGGAGAGCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGC  
TCCCTATGACTGGCGCCGAGCCCCAAATGAAAACGGGGCCCTACTTCTGGCCCTCCGCGAGA  
TGATCGAGGAGATGTACCAGCTGTATGGGGGGCCCCGTGGTGTGGTTGCCCACAGTATGGGC  
AACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGTATATCCG  
GGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTT  
CAGGAGACAACAACCGGATCCAGTCATCGGGCCCTGAAGATCCGGGAGCAGCAGCGTCA  
GCTGTCTCCACCAGCTGGCTGCTGCCCTACAACCTACACATGGTCACCTGAGAAGGTGTTCTGT  
GCAGACACCCACAATCAACTACACACTGCGGGACTACCGCAAGTTCTTCCAGGACATCGGCT  
TTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGGAAGCCACGATGCCACCT  
GGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACTATGA  
GAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGACGGCGATGGTACTGTGAAGTTGA  
AGAGTGCCCTGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTGCAGGAG  
CTGCCAGGCAGCGAGCACATCGAGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACG  
TGTGCTCCTTGGGGCCCTGACTCCTGTGCCACAGGACTCCTGTGGCTCGGCCGTGGACCTGCT  
GTTGGCCTCTGGGGCTGTGATGGCCACGCGTTTTCGAAAGTTTGTGACTCACCATTCAAGG  
CCCCAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTATCCTTTCTCTGT  
TGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAAATGCT  
GCTGATGGTGGAACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCCCTG  
GTCCCAGTCCCTGCCTGGGGCCATGTGTCCCCCTATTCTGTGGGCTTTTCTACTTGCCTA  
CTGGGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTTACTGGGCTGTGGTCTGTACCCAG  
AGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCCCTTCCCACACACCAGCCACAGATAG  
GCCTGCCACTGGTTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAG  
CCTGACTGGCTTCTTGGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTTCT  
TCGTGGTTCCCAGGCCCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCAT  
TCAAGCTCTGGATTGGGCAGCAGATGTGCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCT  
GATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGCCTCCCTTACCCTGGGACTGT  
GGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGAGAAAGGGA  
ATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCCAC  
CATCACACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAG  
GATGGGGCTCCTATCCACCCTGGCCAGCAGCCAGCTTAGTGCTGGGACTAGCCAGAACTT  
GAATGGGACCCTGAGAGAGCCAGGGGTCCCCTGAGGGCCCCCTAGGGGCTTCTGTCTGCCC  
CAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGTCAGGGCTGCCTTCATGGC  
AGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGTGGGGT  
TCCCAAAGACGCCTTACGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGAT  
TTTCTCTGTGTCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGG  
GCTCTGAGCAGGCTGTATCTGGATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAAAA  
AAAAAAAAAAAAA



**FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189  
><subunit 1 of 1, 412 aa, 1 stop  
><MW: 46658, pI: 6.65, NX(S/T): 4  
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL  
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

**Important features:****Signal peptide:**

amino acids 1-28

**Potential lipid substrate binding site:**

amino acids 147-164

**N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

**Lipases, serine proteins**

amino acids 189-201

**Beta-transducin family Trp-Asp repeat**

amino acids 353-365

60/237

**FIGURE 60**

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGACGCGCGGCGACGCGGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACCTGCCA  
GGCCCTCTCTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGGCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTCATGGCACTTCCTCCTTG  
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

**FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304  
<subunit 1 of 1, 224 aa, 1 stop  
<MW: 24810, pI: 4.75, NX(S/T): 1  
MESGAYGAAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIVIGDLLFSALWTFLWVGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

**Important features:****Type II Transmembrane domain:**

amino acids 24-43

**Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

**N-glycosylation site.**

amino acids 97-100

**FIGURE 62**

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGT  
GAGCAGAAGGATGCCCCGTGGCCGAGGCCCCCCAGGTGGCTGGCGGGCAGGGGACGGAGGTG  
ATGGCGAGGAAGCGGAGCCAGAGGGGATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCC  
CGGGGCTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTGGCCCTGCTCGTGCTGGCTTCGGC  
GGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGCCAGGTGTACT  
CAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCCAGGATCTTACCCGCCGGGAATCTAGT  
GCCTTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCG  
CCTGGGAACCTTACTACAACCTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCT  
TCTTCTGGTTTCATTCTCCAAATCCCCGAGCACCGCCGGCTGATGCTGAGCCCCGAGGTGGTG  
CAGGCAGTCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGCTCGGCTGCCGTCCCCACAG  
GGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAAGACATAG  
CTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCCTC  
CGGCTGAAGGGGCCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGA  
CCTCATGCTCAAACCTCCGGCTGGAGTGGACGCTCATCACCTCGGTGTACGGCTGCAGCCGCCAG  
ATGACCTGGCCGGGCCCTGGAGAAGAGGCTCATCACCTCGGTGTACGGCTGCAGCCGCCAG  
GAGCCCGTGGTGGAGGTTCCTGGCGTCCGGGGCCATCATGGCGGTTCGTGGAAGAGGGCCT  
GCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGTGAAG  
TGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCTCAGCACCCCGTACTTCCCC  
AGCTACTACTCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGG  
CTTGGCCCTCTGGTTTGATGCCTATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCC  
AGGGCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCCTACGCC  
GAGAGGATCCCCGTGGTGGCCACGGCCGGGATCAACATCAACTTCACCTCCCAGATCTCCCT  
CACCGGGCCCCGTGTGCGGGTGCATATGGCTTGTACAACAGTCCGACCCCTGCCCTGGAG  
AGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCC  
AACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCAC  
ATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTTGTCTCAACGGCAGCGATGAAG  
AGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGGAGCTGC  
GTGAAGAAGCCCAACCCGCACTGTGATGGGCGGGCCGACTGCAGGGACGGCTCGGATGAGGA  
GCACTGTGACTGTGGCCTCCAGGGCCCTCCAGGTTCCGGGTTCGACACATCTGTGGGGGGGCC  
AGGGTGAGTGGCCATGGCAGGGCCAGCCTCCAGGTTCCGGGTTCGACACATCTGTGGGGGGGCC  
CTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTC  
CACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGG  
TGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCATGACTAC  
GACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCCGCCGTGCGCCCCGTCTG  
CCTGCCCCGCGCGCTCCCACTTCTTCGAGCCCGCCCTGCACTGCTGGATTACGGGCTGGGGCG  
CCTTGCGCGAGGGCGGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCACTTGATCCCA  
CAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTA  
CCGCAAGGGCAAGAAGGATGCCTGTAGGGTGAATCAGGTGGTCCGCTGGTGTGCAAGGCAC  
TCAGTGGCCGCTGGTTCTTGCGGGGCTGGTCACTGGGGCCTGGGCTGTGGCCGGCCTAAC  
TACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTGACCTG  
AGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGCAACTGC  
CAAGCAGGGGGACAAGTATTCTGGCGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGG  
AGGTGGCATCTTGTCTCGTCCCTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGC  
CAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACCCAGGCCACACCCAGCCCTTCTGCCTCC  
CAATTCTCTCTCCTCCGTCCCCTTCTCCACTGCTGCCTAATGCAAGGCAGTGGCTCAGCAG  
CAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGGCT  
GTTTGGGCAGCCTTGCCCTCCAGAGAGCAGATTCCAGCTTCCGAAGCCCCCTGGTCTAACTTGG  
GATCTGGGAATGGAAGGTGCTCCCATCGGAGGGGACCCTCAGAGCCCTGGAGACTGCCAGGT  
GGGCTGCTGCCACTGTAAAGCCAAAAGTGGGGAAGTCCCTGACTCCAGGCTCCTTGCCCCAC  
CCCTGCCTGCCACCTGGGCCCTCACAGCCAGCCCTCACTGGGAGGTGAGCTCAGCTGCCC  
TTTGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRFHSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRLKGPDLASSCLWHLQGPDKDML  
KLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLTSPYFPSYYSPTHCWSHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDCGQPDCLNGSDEEQCEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGCRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWQPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMSTVL  
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCEAYRYQVTPRMLCAGYRKG  
KKDACQGDSDGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQVVVT

**Important features:****Type II transmembrane domain:**

amino acids 46-67

**Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

**N-glycosylation sites.**amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512**Kringle domains.**

amino acids 746-758 and 592-609

**Homologous region to Kallikrein Light Chain:**

amino acids 568-779

**Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

**FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCCTATGGCTTGTACAACCAAGTCGGACCCCTGCC  
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGC AAAGAGGA  
CAGCACATGCATCTCACTGCCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCCAACCCGCASTGTGATGGGCGGCCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGGCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCCGGCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGA CTGAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

**FIGURE 65**

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTAA  
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTCACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCGGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTGAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCCT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFPGPEGRLEDKLHKPKATQTEVKPSVRFNLRSTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDVANNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFFKKGICLS  
CRKNRCSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139



**FIGURE 67**

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCT  
TCCCCCCCCGCTTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCA  
CCCCGGCCGGCCCTGGGGGCTGACAGTCGGCAAAGTTTGGCCCCAAGAGGAAGTGGTCTCAAA  
CCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCGCTGCCTGCGGGCGGGCTGTAGGC  
GAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAGAGAAGAGTGC  
GGCGGCGGACGGAGAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTG  
CCGCCGCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGC  
CCCCCTGGGGAGGCGGCACACAGGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCCATCGGG  
TAGACCACAGAAGCTCCGGGACCCCTCCGGCACCTCTGGACAGCCCAGGATGCTGTTGGCCA  
CCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAGACCGGATTATTTTCCAAAT  
CATGCTTGTGAGGACCCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGAGGCCCT  
GGTCCGGGACAGCCGACCTCCCTGCCAAGTGCACCTGGCTCATCTGGGCGAGCAAGGAAC  
AGACTGTCACCATCAGGTTCAGAAAGCTACACCTGGCCTGGCTCAGAGCGCTTAACCTTA  
CGCTCCCCCTCTCCAGCCACTGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGGC  
CGGGGGCAACGTACCATCACTTACAGCTATGCTGGGGCCAGAGCACCCATGGGCCAGGGCT  
TCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAGAGTTTCAGTGCCTGAAC  
CACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTGTATGCCTGTGGCGATGGCTCTGA  
TGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCCTCCTGC  
CTTGCAATGTCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTA  
GCCTCAGTCTCCACCCCCAGTCTGCCATTGGCTGTGAGCCCCCATGATGGCCGGCGGCT  
GGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTGGAGATGCAGTGCATGTGTATGACGGCC  
CTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCAGCAATGGCAAGGCT  
GTCAGTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCAA  
TGGTCTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCT  
GTGGCTTAGGCTCTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGGGCCA  
CAGCGCTGTGACGGCTCATGGGACTGTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTG  
CCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCTCTGGTGCCACAGCCTGCTACCTGC  
CTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGAGACGCTGTCCG  
CATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCTGTATGAGACGTGGGTGTG  
CGATGGGCAGCCAGACTGTGCGGACGGCAGTGTGAGTGGGACTGCTCCTATGTTCTGCCCC  
GCAAGGTCAATACAGCTGCAGTCATTGGCAGCCTAGTGTGCGGCCCTGCTCCTGGTTCATCGCC  
CTGGCTGCACCTGCAAGCTCTATGCCATTGCGACCCAGGAGTACAGCATCTTTGCCCCCT  
CTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCCCCTTCTACGGGCAGCTCATTG  
CCCAGGGTGCCATCCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATAACTCAGTG  
CTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGAGGTGAGGCC  
AGGTGCCCCGCGTCTGTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGCT  
GGGGCTTGCTCCCTCGAACCACACCCCCGCTCGGGCCTCTGAGGCCAGATCCCAGGTCACA  
CCTTCTGCTGCTCCCCTTGAGGCCCTAGATGGTGGCACAGGTCCAGCCCGTGAGGGCGGGGC  
AGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCAAGGCTCCCCTCCCATCTG  
CTAGACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCACTGCCC  
CTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCT  
GGGGCCCCCAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAG  
ATGAGGACGATGTGCTACTGGTGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAG  
GATGAGCCACTGCTTACCTGAGGGGACCTGGGGGCTCTACTGAGGCCTCTCCCCTGGGGGCT  
CTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCTCCACCATTCTTCCCT  
GTCCCTGGATTTTACGGGACTTGGTGGGCTCCCGTTGACCCTATGTAGCTGTATAAAGTTA  
AGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACA  
CCCCAGTCCCTTACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAA  
AAGTAAAGTTCTTAGAGGATCATAGGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAA  
AGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGACCCTCCAGCCCCCAAGGGGAGGATT  
TGGGCAGAACCTGAGGTTTTTGCATCCACAATCCCTCCTACAGGGCCTGGCTCACAAAAGA  
GTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAA  
AGGAATCATACATCTC

**FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQORPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLSRPLQPLISLCEAPPSPQLPGGNVTTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVTLEDIFYGVFSSPGYTHLASVSHQPQCHWLLDPHDGRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVS YHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGPTRSPFPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

**FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

**Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

**FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

**FIGURE 72**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCGGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGCTAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTTCAGC  
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGCTTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAACTTCATTCTAA

**FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493  
><subunit 1 of 1, 518 aa, 1 stop  
><MW: 56180, pI: 5.08, NX(S/T): 2  
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLR  
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIIYLRDENSRSRFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLPLFRC  
QRRPRDPEVVNDESSLVRHRWK

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 466-494

**N-glycosylation sites.**

amino acids 170-173 and 366-369

**Leucine zipper pattern.**

amino acids 10-31 and 197-118

**Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

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**FIGURE 74**

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCGTGC GGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG  
TCAGGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCACTTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCCTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGGCCACTGGCGTCACCTGCTATGCAGCCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG  
CGCCCATTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACCTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAAA



**FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGA YVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTLLLPCLKACAPSRVVVVASAAHCRGRLDKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL  
AGLGPGEDEAPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP  
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

**FIGURE 76A**

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGG  
AGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGG  
GCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCACCTCCACCATCCGCTGG  
TTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCTGCCTGATGG  
GACCCTTCTGCTGCTACAGCCCCCTGCCCCGGGACATGCCACGATGGCCAGGCCCTGTCCA  
CAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC  
GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGCC  
TGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCCGCCCTGGGGCCACCCAGAGCCCACAG  
TCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCAGGACACACAGTGTCCGGG  
GGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGGACCTACATGTGTGTGGCCAC  
CAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCCGGGTTTCCATCCAGGAGCCCCAGGACT  
ACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAATGTGACACTGCTGAAC  
CCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTCAGTGG  
CCCTGCTGCGCCTGCCAATCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCC  
AGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCCGGCTGGCAGAGCGCAGAGCTTGGAGGCCCTC  
CACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGCCGGGCTCGAGGCCCTGA  
CAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGAGTGGCCAGTGGCCACCTCAGGAAGTGA  
CTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAC  
AATGGCATCATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAA  
CTGGACTGTAGTTGGTGAGCAGACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACT  
GCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCTGGGGAGCCAGTAGACCTGTCTGCCTC  
CTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCCAGTGAGCATGGTCCCTGGACCCT  
GGAGCAGCTGAGGGCTACCTTGAAGCGGCCCTGAGGTCAATTGCCACCTGCGGTGTTGCACTCT  
GGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACTTG  
GGCCAGGTCTGTACAGATATACCAGTGAGGATGCCATCCTAAACACAGGATGGATCACAG  
TGACTCCCAGTGGTTGGCAGACACTTGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCA  
GCAGCAGCCTCAGCAGTCGGCTGGGGGCGGATGCCCGGGACCCACTAGACTGTCTGCTGCTCC  
TTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCCTGCTTCCAGACACCAGCACTTTTTA  
TGGCTCCCTCATCGCTGAGCTGCCCCCTCCAGTACCCACAGCCAGGCCAAGTCCCCAGGTCCCAG  
CTGTACAGCGCCTCCACCCCCAGCTGGCCCAGCTCTCCAGCCCCCTGTTCCAGCTCAGACAGC  
CTCTGAGCGCCGAGGGGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGGAA  
GGCCAAAAGAAGCAGGAGCTGCAGCATGCTCAACAGTTCCCCACTGCTCCGGGGCAGCCACT  
CCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTCCAAGAACCTTTCCCAAGCCCCA  
GGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTTCCAGCTCCTC  
AAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTCTTTCCCTCATGAAACTCCCCAA  
CTCAGAGTCAACAGACCCAGCCTCCGGTGGCACACAGGCTCCCTCCTCCATCCTGCTGCCA  
GCAGCCCCCATCCCCATCCTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTC  
TGGCCCCAGCCCAGCTTCCAGTCGCCTGTCCAGCTCCTCACTGTCTATCCCTGGGGGAGGATC  
AAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAACTCAGTGAGGGTGAGGAG  
ACTCCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTCACCCCCACCACCTATGGGTA  
CATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGC  
CCAAGGGGGGAGTCTTGCTGTGCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGC  
TCCTTAGCCAATGGTTGGGGCTCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCT  
TGTGAGCTCCTCCGATGGCTCCTTCTCGTGTATGCTCACTTTGCCCCGGGCCCTGGCAGTGG  
CTGTGGATAGCTTTGGTTTTCGGTCTAGAGCCCAGGGAGGCAGACTGCGTCTTCATAGATGCC  
TCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCCCTGTG  
GGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGCTGGGAAGGG  
GGATGCCTCCCTGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGT  
ATGCCCAAGGCTGGTGCTTCTCCTGTAGATTACTCCTGAACCGTGTCCCTGAGACTTCCCAG  
ACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAGACCTGGGCTGTGGTGTGTGGGTCTT  
GGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAGTTCTCCCTCCAC  
GATTGTGAAAACAAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAA  
AACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCAC  
CAGGTTGTTTTGGCCTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCACCATTGGATCACA

**FIGURE 76B**

GGAAGTGGAGGAGCCAGAGGTGCCTTTGTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGT  
GGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCTGGGCCCCCTCCTCTAGAGAAGAG  
CTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTGAGGCACTGA  
GGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGG  
GAGGTATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAA  
ATTTGATACCATAAAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404  
<subunit 1 of 1, 985 aa, 1 stop  
<MW: 105336, pI: 6.55, NX(S/T): 7  
MGGMAQDSPPQILVHPQDQLFQGPGRMARMSCQASGQPPPTIRWLLNGOPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLRLPEKVPSPAPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGWP  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPAVRRLLPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA  
WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQTPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS  
LSGSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPDPDSQISSQRSQLHCRMPKAGASPDVYS

**Important features:****Transmembrane domain:**

amino acids 448-467

**N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

**N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

**Phosphotyrosine interaction domain proteins**

amino acids 740-753

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**FIGURE 78**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTTGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA  
ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCTCCCTCCCCTTCTCCAC  
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC  
TGGATCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGTGCTGAGCCTTCTGTGAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAGGAAGCC  
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG  
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCA  
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
CTCATGCCCAGTGTGCGACCCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT  
GTGAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG  
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTGGTAAAGTA  
GCACAACTACTATTTTTTTTCTTTTCCATTATTATTGTTTTTAAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCAGATCTGCAACTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTGAGTATGCAAACTTGGAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
TTTACAGAGCAATTATCTGTATATACAATTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

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**FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196  
<subunit 1 of 1, 332 aa, 1 stop  
<MW: 36143, pI: 5.89, NX(S/T): 1  
MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG  
TSQYGHERTSQYTGTSPPHATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWSRLTAEKEAPSQAPEGD  
VISMPPLHTSEEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

**FIGURE 80**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

**FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCNSNLTPNVNVCRCMYCSDLLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107



**FIGURE 82**

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTGCTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT  
GGAGAAGTGC GGCTGTGACAGGACAGTG CATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGTTGGGCACGAGGGGCGGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCTACTGGTGTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

**FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPLVFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 88-91 and 297-300

**Wnt-1 family signature.**

amino acids 206-215

**Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

**FIGURE 84**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACCTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

**FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352  
<subunit 1 of 1, 293 aa, 1 stop  
<MW: 32562, pI: 6.53, NX(S/T): 2  
MDTTRYSKWGGSSSEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLRLTNASKQTAALGALKKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:****Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 86**

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGTCTTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAGAACCCAGCCCCGGCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCCTCTCCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCTGCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCCGCAGCCCCCTGGGGCCCCCG  
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCTTCATCG  
TCCAGGGGCCTGGCTCCCAGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971  
><subunit 1 of 1, 331 aa, 1 stop  
><MW: 35844, pI: 5.45, NX(S/T): 2  
MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLCLCDGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRGLGTSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

**FIGURE 88**

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAACATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGAGAAATTTT  
ATCCAACTTTGTTTGGAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTCGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAAGCAAGACAATTAAAACGGGAAGTCTTAGCAG  
CAAAACAAAAAAGTAGAAATGCAGCAAAACAAGCAGAAAAAGAAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAAGTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTTCT  
TCCACAAAAA

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**FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919  
><subunit 1 of 1, 472 aa, 1 stop  
><MW: 53847, pI: 5.75, NX(S/T): 2  
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNVRVSQSMKGKSKSSHLLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMShVLQFEDKSRKV  
DASMQSDTFEIYDPRNPVNKRREESKKLMREKKERR

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

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**FIGURE 90**

CGCCGCCGTTGGGGCTGGAAGTTCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTGCGCTTGCTGACGGCGTCCG  
AGCCCTGGCCAGACAATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTCCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCCTCAAGTGGTCACCAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT  
TCTCCAGACCTCCTCTAGGTATCCTCAGSTTTCACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG  
TGCAGTGGCAGCATCTCGGCTCACTGCAACCTCCGCTCCCGGGTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
ATGTACGTACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCGC  
GAGAAAGTGGTGTGGTGTCTTGCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCCTGTCGGCCAGTCCGGC  
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCCCAGAGTGGCACCGCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTGCCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCCTTGGTGTCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGCAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTCAAATCCT  
CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTATACCATCCATCCTGCTCAACCTTGTCTGTCTGT  
TCACATGGCCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

**FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179  
<subunit 1 of 1, 545 aa, 1 stop  
<MW: 58934, pI: 9.45, NX(S/T): 4  
MSTGFSFGSGTLGSTITVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG  
FGTGLFSGKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRETRYKWLRFSEDCLYLNVEYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD  
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

**Important features:****Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

**FIGURE 92**

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGA  
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAATGAGCACCCGGGGCC  
GATTCCAGTCACTGGGGATCCCGCCAAGGGGAAGTCTCCTTGGTGATCAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACTTCTTTTGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTACGTGACAACAC  
GCCAGCCCTGGAGCCCCAGCCCCAGGGAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT  
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGTCAG  
AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCG  
GGTGAAGGCTGGGGATTACAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCAGC  
AGCGAGCCCTGGACCTCTCTGTGTCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
GCAAACAGGACAGTCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT  
CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGT  
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCCAGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
AAGCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG  
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAAACCCAAATCATCCACTCAAGC  
CCCAGAATCCCAGGAGAGCCAAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCA  
GACCCAGGCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTC  
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTTCCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC  
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTCGAGACCAGCCTG  
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG  
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAGATCACACCATTCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
TCTCAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA  
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC  
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCCAGCTGT  
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA  
ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCACTGCTACACTCCT  
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCCACCCCTTGTGTTAGCAAATAAGCAAGAAATAACCATAAAA  
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT  
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA

**FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 60268, pI: 9.53, NX(S/T): 3  
MLLP LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSF SYPRQDWTGSTPAYGYWFK  
AVTETTTKGAPVATNHQSREVE MSTRGRFQLTGDPKGNCSLVIRDAQM QDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARM PKGTQADYAEVKFQ

**Important features:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

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**FIGURE 94**

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTCTATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACTTTAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT  
GATTGCGAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTAA  
AAAGAAAGTGGATTTTGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCCCTCCTTCCATATTATGTATTTGAAGTTTTGA  
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGAGATAGAGATGAATCCATAGAGACACCATTT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTCATTATGATCATA  
TTTGGGTTTTATTTTTTTGACTTTGGGTTTTAAACAACGGAGAAAACAGATTCTATTTCCTGA  
GAAAAGTGAAGATTTCAAGAGAGATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCACTTTTGAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGGAGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTTTACCATCAAATTTTTAAAAGTGCTAATGTGTATTGCAACCCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTGATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG  
TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT  
TTAA

**FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLLRFMLGIPLLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD  
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHFFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRGTGENLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVDCDGS GSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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**FIGURE 96**

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGCAAACATTTGACATTATT

**FIGURE 97**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGCGGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCCTTGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACCACAGAGGCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAAATGGACATTGAGATACTATCATTAAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAA  
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA  
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAAT  
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
TTATATACATATGTAACAGTCAAATATCATTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCACTCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTA  
GTTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACCTTGGAGGCAATCTTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAAACT  
ACCTTTTTTGTCCCCATTCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCCTTCCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
GTGGTTCAAGTGCCTTCCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCTTCCCTCTCTCTACCAGTCTATTTCCATTCTTTTCAGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTTGGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG



**FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAI VSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQI  
QCKVFDSLNLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPV NARYEFGQALFTGWAAASLCLLG GALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKDYV

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

**N-glycosylation site.**

amino acids 72-75

**PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

**ABC-2 type transport system integral membrane protein**

amino acids 119-133

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**FIGURE 99**

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCCTGTCCC

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**FIGURE 100**

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

**FIGURE 101**

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTTCTGCGA

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**FIGURE 102**

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

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**FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTGTCCCCGAA

**FIGURE 104**

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTCCTGCGAACC

**FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTG

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**FIGURE 106**

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAACAACCTCTTACCCACG

**FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGCGAA

**FIGURE 108**

CGGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCCG  
ACCGGTCCCCGCCTTTTGTAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCTGAGCCTCGAGCCGCGAGCAGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTGTCTCCAAGTACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT  
GATAAACCACATGATGTAGAAATAAAATAAAATTATATCCACAACATGATCAAAAGCAGAAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTG  
CTTCCGTGTCTTCAGTTCGTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTTAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGACAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTCACTAAATAACAACGTGTCATAGGGAGGGAAATTCCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCGTTTGA  
CTATGTAGCATCTTGAAAGAAAAATTATAATAAGCCCCAAAATTAAGAAAA

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**FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977  
<subunit 1 of 1, 243 aa, 1 stop  
<MW: 27228, pI: 7.43, NX(S/T): 2  
MAKVEQVLSLEPQHELKFRGPFDDVVTNLKLGNPDRNVCFKVKTAPRRYCVRPNSGIID  
AGASINVSVMLOPFDDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIISTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

**Important features:**

Putative transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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**FIGURE 110**

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTGTCATTTTGTACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

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**FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

**FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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**FIGURE 113**

GGTGGCCCATTCCTCGGCCAGGCTGCTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTCAANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGT  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAAGTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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**FIGURE 114**

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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**FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTcantt  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTcagagatg  
TTTAATGCATATTTAANTTATTTAATGTATTTcatntcatgTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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**FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGCTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

**FIGURE 117**

GCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCACTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTCCACC  
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTCACTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
TATCTGTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCACTGATCTTGGACAAA  
AGGTTCTTAACCAATTTCCCTTTCAAGCAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAGGACTATG  
TCAAAGGGAGTAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTTC  
AGAGGATTGCCGAAGGGAGGCCTTCCTTTCACTGGACCCGGGTCAAGAATACCCACATTTCCG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCACAAAAGAAATACATGGAATCGAATCAGCCCAACGATCAAGAAAA  
TGCTTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATGAGTTGGTCTAT  
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAAGAGGAC  
TACAACGTTGCTGTTGCGATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTACGG  
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGATGAGTTTCATTTGTAGAAAAATTTGTTGCCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCACTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTGTGTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTTAGGACAAAGAATTCTGTAATCTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

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**FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253  
<subunit 1 of 1, 413 aa, 1 stop  
<MW: 47070, pI: 9.92, NX(S/T): 3  
MENMLLWLIFFTPGWTLDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPOHVLTAACHVHDGKDYVKGSKKLRV  
GLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDENDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93; 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

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**FIGURE 119**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCACTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCAATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTT  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTTGATCACTT  
ATATCTGGAAACCAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTTATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAAA

**FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847  
<subunit 1 of 1, 525 aa, 1 stop  
<MW: 58416, pI: 6.62, NX(S/T): 1  
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAGPWSECSRTC GGGASYSLRRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPNCSLKQC  
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLGPDHLYLETCTLQGTKGENSLSSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPSC  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKL PVEAKLPWFKQAQAELEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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**FIGURE 121**

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGCGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCACTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCCGAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAATTTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC



**FIGURE 122**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELROAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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**FIGURE 123**

GGGGATTGTAAAGAGGAAGNACTGTGCCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATACTGGGCA  
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

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**FIGURE 124**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCC  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAAACTTG  
AAAAACAGTTTGTAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKEYR  
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI  
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLPGLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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**FIGURE 126**

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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**FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTTACTCCTGTAACAAC TGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTTATGCTGACTGGTGTGCTTTTCAGTCAG  
ATGTGGCATCCAATTTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

**FIGURE 128**

GCCCACGCGTCCGATGGCGTTACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTAAGTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAAGTGTGACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACCTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT  
GCAATACAATAAACTCTGAAATTAAGACTC

**FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

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**FIGURE 130**

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG  
AATCCCCTTGTTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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**FIGURE 131**

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAATTCCTCCTCATAGAGCTTTTAAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

**FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP  
KEEELYACQRGCRFLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHLLFPLTLVRSFWSMDMSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLMRNSQAHNFLEDGESDGFRLCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

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**FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG  
TGAAGTGAAGACAAGAACAACCTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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**FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTGCGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

**FIGURE 135**

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTGAGTCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACCTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGATTTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCCTTCGAGCGCCCGAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTTG  
CATTTTGATGAGAATTCATTTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC  
TCAGGAACCTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPETAQAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDFRYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPGIIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 280-283 and 384-387

**Amidation site.**

amino acids 94-97

**Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

**Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

**Interleukin-7 proteins**

amino acids 338-343

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FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCCAGATTTTCAACTNNTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTTCCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG



**FIGURE 138**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGTATGGGGGATT  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTGAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAATAATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGGCCAAG  
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

**FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

**FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACCTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

**FIGURE 141**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTTCGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTACCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCATAGGTTTTGCGGAAGGGCCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAACAC  
TGA CTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGAGAGCCCCACTTTCCAGATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGA ACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTTC  
TGTTGGTAAAGTACAGAATTACAGCAATAAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAA

**FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033  
<subunit 1 of 1, 311 aa, 1 stop  
<MW: 35076, pI: 5.04, NX(S/T): 2  
MQFTTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSTNMKHLIMWSPVIAIGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPFQFEFLVAYWRREPAAEEHV  
KMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALFAFVGEM  
LILV  
VVPFLVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPE  
ELLRAWIS

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation site.**

amino acids 40-43 and 134-137

**Tissue factor proteins.**

amino acids 92-119

**Integrins alpha chain proteins**

amino acids 232-262

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**FIGURE 143**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATAACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 144**

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCGAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAAGTCTACGGGAATTTAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTC  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCGCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

**FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353  
<subunit 1 of 1, 328 aa, 1 stop  
<MW: 36238, pI: 9.90, NX(S/T): 3  
MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSLTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 177-199

**N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92



**FIGURE 146**

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCC  
GCCGCCGAGCCTCGTTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGG  
GGCGCCACCCTGGCAGACTAACGAAGCAGCTCCCTTCCCACCCAACTGCAGGTCTAATTT  
TGGACGCTTTGCCCTGCCATTTCTTCCAGGTTGAGGGAGCCGCAGAGGCGGAGGCTCGCGTAT  
TCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTCGCGAGCGGGG  
CTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGCGCTCCGGTTTG  
GCTCACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGG  
AGATTTTCTGGGGAAATCCTGAGGTCATTATTATGAAGTGACCGCGCGGGAGTGCGTCA  
GAGTAACCACAGTGTGTTTCATGGCTAGAGCAATTCCAGCCATGGTGGTTCCCAATGCCACT  
TTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGTGAGTGGTGGATAGCCAAACA  
ACGAGGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCATAATAAAT  
TACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTG  
GAAAGATCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCT  
TCCATCAATTGGACAGAATTTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATG  
TACAATCGTGGTATGATGAAGTGAAAGACTTTAGCTACCCATATGAACATGAATGCAACCCA  
TATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACACAGGTGCTGTGGGCAAC  
TAGTAACGAATCGGTTGTGCCATTAATTTGTGTCTATAACATGAACATCTGGGGGCGAGATAT  
GGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCC  
CCTTACAAACATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTGGAGGGGGCTGTAGAGA  
AAATCTGTGCTACAAAGAAGGGTCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATG  
AAATAGAACGACAGCAGTCACAAGTCCATGACACCCATGTCCGGACAAGATCAGATGATAGT  
AGCAGAAATGAAGTCATAAGCGCACAGCAATGTCCCAAATTGTTTCTTGTGAAGTAAGATT  
AAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGATA  
GTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCA  
ATTCAATTATGGTATAATAGACAAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAA  
GCATTATTTTCATCAAGTCCAATAGAAATGGTATTCAAACAATTGGCAAATATCAGTCTGCTA  
ATTCCTTCACAGTCTCTAAAGTAACAGTTTCAGGCTGTGACTTGTGAAACAACCTGTGGAACAG  
CTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCTCGTAACTGTAT  
GCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTTTATTCTGATCTGTCCAGTA  
TCTGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATG  
CCTGTGGACAAAAGAAAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTT  
ACAGAATCCTCCAGGAGGAAAGGCATTACAGAGTGTGTTGCTGTTGTGTGAAGTGAATACTTG  
GAAGAGGACCATAAAGACTATTTCCAAATGCAATATTTCTGAATTTTGTATAAACTGTAACA  
TTACTGTACAGAGTACATCAACTATTTTCAGCCCCAAAAGGTGCCAAATGCATATAAATCTT  
GATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAATAT  
AATGGTTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTT  
AATTACATAGTCATGATTGTTCTACGTTTTCATATATTATATGGTGCTTTGTATATGCCACTA  
ATAAAATGAATCTAAACATTGAATGTGAATGGCCCTCAGAAAATCATCTAGTGCATTTAAAA  
ATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTTCCCCAGTTCAATGCTATGCCAT  
TACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTTCTGTTA  
ATTTAGGCATATAGAATATTAAATCTGATATTGCACCTCTTATTTTATATAAAATAATCCT  
TTAATATCCAAATGAATCTGTTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATG  
TAATAAAGTCAGAGTGGTGGTATGAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTA  
AGCATGGACAGCCAGAGCTTCTATGTACTGTTAAATTTAGGTCACATATTTTCTTTTGTA  
TCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTTGAACAAAGATGAAC  
AATGTATTACATTACCATTGCCACTGATTTTTTTTTAAATGGTAAATGACCTTGTATATAAAT  
ATTGCCATATCATGGTACCTATAATGGTGATATTTGTTTCTATGAAAAATGTATTGTGCT  
TTGATACTAAAAATCTGTAAAAATGTTAGTTTTGGTAATTTTTTTCTGCTGGTGGATTACA  
TATTAAATTTTTCTGCTGGTGGATAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAA

**FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417  
<subunit 1 of 1, 500 aa, 1 stop  
<MW: 56888, pI: 8.53, NX(S/T): 2  
MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLLEKYMDEDEGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCFRCSGPVCTHYTQVWVWATSNRIGCAINLC  
HNMNIWQGIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFSGGCRENL CYKEGSDRY  
YPPREEETNEIERQSQVHDTHVTRSDSSRNEVISAAQMSQIVSCEVRLRDQCKGTTTCNR  
YECFAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHFIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCFHKKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

**Important features:****Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

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**FIGURE 148**

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCTGCTCCACGCGCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGCTGGCGTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGAAAACCTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAAAAGCCTTTTACCAACGGTCAG  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA  
GGAACAATGAGCTTGGTGGACACATTTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAAC  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTAAACAGTGCAGTCCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTGAAATGTAAAA  
AAAAAAAAA

**FIGURE 149**

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**FIGURE 150**

CCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCATGTTAAACTCCA  
ATGTCCTCCTGTGGTTAACTGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAAGCACAG  
TATCCAGTTGTCAACACAAATTATGGCAAAATCCGGGGCCTAAGAACACCGTTACCCAATGA  
GATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCATGCTTCACCCCCCACTGGAGAGA  
GGCGGTTTCAGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAAATACTACTCAGTTT  
GCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTG  
GTTTACCGCCAATTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTT  
ACTTAAACATCTACGTGCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATA  
ACGAGTAATGACCGTGGTGAAGACGAAGATATTATGATCAGAACAGTAAGAAGCCCGTCAT  
GGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAACATGATTGACGGCAGCATTT  
TGGCAAGCTACGGAAACGTATCGTGATCACCATTAACTACCGTCTGGGAATACTAGGGTTT  
TTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACT  
GCGGTGGATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTG  
GCTCGGGGGCTGGGGCCTCCTGTGTGACGCTGTTGACCCGTGCCACTACTCAGAAGGTCTC  
TTCCAGAAGGCCATCATTAGAGCGGCACCGCCCTGTCCAGCTGGGCAGTGAAGTACCAGCC  
GGCCAAGTACATCGGATATTGGCAGACAAGTTCGGCTGCAACATGCTGGACACCACGGACA  
GGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCCGGCC  
ACCTACCACATAGCCTTCGGGGCGGTGATCGACGGCGACGTCTCCAGACGACCCCCAGAT  
CCTGATGGAGCAAGGCGAGTTCCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAG  
GCCTGAAGTTCGTGGACGGCATCGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGAC  
TTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGGCTACCTGAAGGGAAAGACACTTTGCG  
GGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCCGGAGACGCGGCGGA  
AAACCCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCCGTGGCCGCGGACCTG  
CACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAAT  
GAAGCCCAGCTGGGCAGATTTCGGCCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCA  
TGATCGGTCCCACCGAGCTCTTCAGTTGTAACCTTTTCCAAGAACGACGTCTGCTCAGCGCC  
GTGGTCACTGACCTACTGGACGAACCTTCGCCAAACTGGTGATCCAAATCAACCAGTTCCCTCA  
GGATACCAAGTTTCACTCACACAAAACCCCAACCGCTTTGAAGAAGTGGCCTGGTCCAAGTATA  
ATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGG  
GCAACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCCTCATTTGCACAACCTGAACGAGATATT  
CCAGTATGTTTCAACAACCACAAAGGTTTCTCCACCAGACATGACATCATTTCCCTATGGCA  
CCCGGCGATCTCCCGCCAAGATATGGCCAACCACCAACGCCAGCAATCACTCCTGCCAAC  
AATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGAGGACACAACCTGTCTCTATTGA  
AACCAAACGAGATTATTCACCGAATTAAGTGTCACCATTGCCGTGCGGGCGTCTGCTCCTCT  
TCCTCAACATCTTAGCTTTTTCGGGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACT  
CACAGGCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGA  
GATCATGTCTCTGCAGATGAAGCAGCTGGAACACGATCACGAGTGTGAGTCTGCTGCAGGCAC  
ACGACACACTGAGGCTCACCTGCGCGCCAGACTACACCCCTCACGCTGCGCCGGTCTGCCAGAT  
GACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAACACACTGACGGGGATGCA  
GCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCACGGAC  
ATTCCACCCTAGAGTATAGCTTTTGGCCCTATTTCCCTTCCTATCCCTCTGCCCTACCCGCTC  
AGCAACATAGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGAC  
CAGGAATGTTTTTGTCCCACTGACTTAAGACAAAATGCAAAAAGGCAGTCATCCCATCCCG  
GCAGACCCTTATCGTTGGTGTGTTTTCCAGTATTACAAGATCAACTTCTGACCCTGTGAAATGT  
GAGAAGTACACATTTCTGTATAAATAACTGCTTTAAGATCTCTACCACTCCAATCAATGTTT  
AGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTGTTCCAACGTATGGAAGCAGCTGA  
CACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATT  
TCTTCTGTGCCACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGC  
CCAGCACATGGAGCTGTAATCCAGAGAGAAGGAAACGTAGAAATTTATTATTAAAGAATGG  
ACTGTGCAGCGAAATCTGTACGGTCTGTGCAAAGAGGTGTTTTGCCAGCCTGAACTATATT  
TAAGAGACTTTGT

**FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG  
VNOGEGCLKFVDGIVDNEDGVTPNDFDFSNSNFVDNLYGYPEGKDTLRETIKEMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEV  
PYVFGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNR  
FEEVAVSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVP  
PPDMTSFPYGTRRSPAKIWPTTKRPAITPANNPKH SKDPHKTGPEDTTVLIETKR  
DYSTE LSVTI AVGASLLFLN ILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEE  
IMSLQMKQLEHDECE SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTFNTITMIPNTLTGMQ  
PLHTFNTFSGGQNSTN LPHGHSTTRV

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GGGAAAGATGGCGCGGCACTCTGGGACCCTTGGGTCTGGCAGCAGTGGCGGGCATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTTCCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCCTACCCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGG  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTGGTGATTTCGCTACGTCAAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCCTGCC  
CCGCGGCTACTACTTCCGCCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCCTTGAAGTTGTTTGAACATGACAGCTGGAGAGAACCCCAAGAGGAAAGACTCCATCGA  
GATGTGTCTTGGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCCGC  
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTAGAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCAGT  
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCTCATGGTTGTGCATGGGGACATCTAACT  
CTGGTCTGGGAAGCCACCCACCCACAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAATTTCATAGCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG  
AATCCAAAGAATAAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTTCGTTGGGTT  
TTGCATTTGACCCAAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAACCAGGATGGAACT  
TCTTCCCTGCGTTACCTTCTTCTTCACTCCATTGATGTCCTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGACACCACTGCGTTTCACT  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
TACGATTTTTTGAATCCCACTTTTGAAGTGTGAAAGTGTAAAGGAAGCTTTCTTCTTACACCT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCTCATCATCTGTGCCTGGAAGAGTT  
CACTGTCATTGAGCAGCACAGCCTGAGTGTCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA  
TTTGACAAGGGGTTACATGTCTGCTCACTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCTTCTGATCAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGCGCGCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCGGCCATGG

**FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911  
><subunit 1 of 1, 348 aa, 1 stop  
><MW: 39711, pI: 8.70, NX(S/T): 1  
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQALWNRVPCFLRDWELQVHFQKHGQKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQQERVFPYISAMVNNGSLSY  
DHERDGRPTLGGCTAIVRNLYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPMTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

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**FIGURE 154**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCCTGGGACCATGGGCGTGAGTGCAATC  
TACGGATCAGTCTCTGATGGTGGGTGCTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAG  
AAAATCAGTTGTCTTCATTCAAGAATTGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAA  
TCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCTGACATGTTCCCGATTTGAGGTGA  
AACCATGAAGAGAAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCTTGCTGCTGCT  
GGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCCG  
TGTCGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTG  
ACGGAGCCCCCTGTGACAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGT  
GGCCGAGCGCAGCATGGAAGGTGATGCCCCGCATCATTTTAAGCTGGTCTCAGTGCAATGTGT  
TCATTGCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCAAACAAAGCGACCAGAAATT  
GACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCATTAGTCA  
CATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTTGAACCTCCTTGCCCTTTTACCCAA  
ATCACCCATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAAC  
GGTCAGCTGCTGAGGGATATCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGC  
AGACAGCTCTATTTAGAGACCACTGGGAAAAGCCGGACCCTACAAAGTGGGCTGGCCTTGC  
TTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTTCAGGCACCAGCCAAGTGGC  
CTGTTCTGCTCTGGAAGCTGCTATTGCCCCGGTAAGAAACCAGTATCTGGAAAAGGAGCAGCG  
TCGTGAGTACCTCCTACGTTTGA AAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCA  
AGATCGTGGATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCTATAGACTCCATGCTCTGC  
CACTTCTGCCACAATGTCAGCTTTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTT  
CAAGGTAATTAAGACCCATCAGATCGAGGATGAAAGGGAAAGACGGGAGAAGAAATTGTACT  
TCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCGGCCGGATGCAGCGT  
GCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGTC  
ACCAGTTCTCAGTGCCTTGGGCCTTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGA  
TCTTTGAGCTTTGGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAAT  
GGCGTCGATGTCACATTCCACACCTCTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCC  
CATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAAGGGACATGTTTGTAGCCCTGGGTG  
GCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTCTAAAGGTATGCAGTACA  
GCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTGCTTTGTCTGTT  
ACTAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGG  
TTGGGGTTGAACAGTAAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGG  
CCAGTTCACAGAGGAATAGAAGGTACTTTATCATAGCCAGACTTCGCTTAGAATGCCAGAAT  
AATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCACCTCTTCTGGCCTGCCCCATGTT  
ACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATTTTACCTT  
GTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTCTGT  
AAAGGGCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTC  
ATAACTACTCAACTCTGTTTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATAT  
GTGTAGCTGGGTTCAGGCCAGACAAAACAGATGGTGACCAGACTTGGCCCCCTGGGCTGTA  
GTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGCACTTCCAGCACTTTGAGA  
ACGAGTTGAATACCAAGAATTATTCAATGGTTCCCTCCAGTAACCTTCTGCTAGAAACACAGAA  
TTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAA  
TCATAGAAAACCTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTT  
AAGTATGTTCTAAATATTTGTCTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTAT  
GCCATTTAGTATTTTTATAGTTTAGGAAAATATTTTCTAAGACCAGTTTTAGATGACTCTTA  
TTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAGGAGGCTAGAAGATGA  
ATTCAGGCACTTCTTCCAATAAACTAATTATGGCTCATTCCTTTGACAAGCTGTAGAAC  
TGGATTCAATTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCCTGATTGATTTTTAAAT  
CGTTTTTGAAGAACCTTGTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATAT  
TAGAAGCAATTATAATTACATCTGTGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGA  
AAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCCAACCTTTTCTCTTTGTTTTGTCCA  
GTGTTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

**FIGURE 155**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329  
><subunit 1 of 1, 480 aa, 1 stop  
><MW: 55240, pI: 9.30, NX(S/T): 2  
MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDVPY  
EALLYCNIPSV AERSMEGHAPHHFKLVSVHV FIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLONGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRROYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMLCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

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**FIGURE 156**

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGA  
ACAGTACTGTGGAGCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTG  
TGCAGTAATTGGTTAGGACTCTGAGCGCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGA  
TCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGATAGCTAGGAATGAACCATCCCTGG  
GAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCACTGTCCCATTCTATGGGCGAAGGA  
ACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAT  
GATTCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGA  
CTCTGTGGGAGACCGGATGCACCCAGATACGCTATTCACTTCCGGAAGAGCTGGAGAAAGGC  
TCTAGGGTGGGCGACATCTCCAGGGACCTGGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGG  
AGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCTGAATCCGCGCAGCGGCAGCT  
TGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTGTCAATTA  
AATCTAGACATTCTGATGGAGGATAAAGTGAAAAATATATGGAGTAGAAGTAGAAGTAAGGGA  
CATTAAACGACAATGCGCCTTACTTTCTGTAAGTGAAATAGAAATAAAAATTAGTGAAATG  
CAGCCACTGAGATGCGGTTCCCTCTACCCACGCCTGGGATCCGGATATCGGGAAGAACTCT  
CTGCAGAGCTACGAGCTCAGCCCGAACACTCACTTCTCCCTCATCTGCAAAATGGAGCCGA  
CGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCGCGAAGAAAGGCTGCTC  
ACCACCTGGTCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCGCATC  
CGCGTGATGGTTCTGGATGCGAACGACAACGCACCAGCGTTTGCTCAGCCCCGAGTACCGCGC  
GAGCGTTCCGGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCCTG  
ACGAAGGAGTCAATGCGGAAGTGAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCCAA  
GTTTTCAAACCTAGATTGTAATTCAGGGACAATATCAACAATAGGGGAGTTGGACCACGAGGA  
GTCAGGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATATTCTGCGCGAGCCA  
AAGTCTTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCTACCTCTCTC  
GCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGA  
TAGAAAAATCTTACGGAAATTACTATAGTTTAGTACAGACATAGTCTTGGATAGGGAACAG  
GTTCTTAGCTACAACATCACAGTGACCGCCACTGACCGGGGAACCCCGCCCTTCCAGGGA  
AACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCCGGTCTTCCCTCAGGCT  
CCTATTCCGCTTATATCCCAGAGAACAATCCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCC  
CACGACCCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACCATCCA  
AGGGGCAAGCCTATCGTCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGA  
GCTCCTTCGACTACGAGCAGTTCGAGACTTGCAAGTGAAAGTGATGGCGCGGGACAACGGG  
CACCCGCCCTCAGCAGCAACGTGTGCTTGAGCCTGTTCTGCTGGACCAGAACGACAATGC  
GCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCTGGCTCCCC  
GCTCCGCGAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAG  
AACGCTGGCTGTCTTACCCTGTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCT  
GCACACGGGCGAGGTGCGCAGCGCGGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCC  
TCGTAGTGGCCGTCCAGGACCAAGGCCAGCCCTCTCTCCGCCACTGTCCAGCTCACCGTG  
GCCGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAGCCTCGAGTCTCCAGCTAA  
CTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCTGCGTCT  
TCCTGGCCTTCGTCTCTTGTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTG  
CTGCAGGCTTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTGCACCTTTGTGGGCGTGGACGG  
GGTGCAGGCTTTCTGACAGACCTATTCACAGAGGTTTCCCTCACCACGGACTCGCGGAAGA  
GTCACCTGATCTTCCCCAGCCCCAACTATGCAGACATGCTCGTCAGCCAGGAGAGCTTTGAA  
AAAAGCGAGCCCCCTTTGCTGTGAGGTGATTCCGTATTTTCTAAAGACAGTCATGGGTAAAT  
TGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTAAATGCTCTGTCTCCCAAGCTG  
GAGTGCAGCGGTACGATCATAGCTCACTGCGGCTCAAACCTCCTAGGCTCAAGCAATTATCC  
CACCTTTGCCTCCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTAT  
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT  
GGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGCGGAGGCGGGTGGATCACCTGAGGTT  
GGGAGTTTGGAGACCGCTGACCAACATGGAGAAACCCCGTCTATACTAAAAAATACAAAA  
TTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAA  
TTGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCT  
GGGCAACAAGAGTGAAACTCTATCTCA

**FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306  
><subunit 1 of 1, 916 aa, 1 stop  
><MW: 100204, pI: 4.92, NX(S/T): 4  
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGEVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFFLP HAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLYALSSF DYEQFRDLQVKVMARDNGHPPLSSNVLSLFLVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD  
GVQAFLQTY SHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNC SVSQAGVQRYDHSSLRPQT PRLKQLSHLCLRCNRDYRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

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**FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTCAAGAGTGCCAACCCCATTCGCAGCCTTGCCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCTTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAAGTCCCCGAGAGAATTTTCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT  
CTGGTTC

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**FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336  
<subunit 1 of 1, 260 aa, 1 stop  
<MW: 28048, pI: 7.87, NX(S/T): 1  
MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEI PVVQSI PHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 160**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGGCTGCGCGCCCGGGCCCGC  
CGCGCCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCGC  
GCCCCGCGCCAGGTGAGCGCTCCGCCCCCGCGAGGCCCCCGCCCGGGCCCGCCCGGCCCGC  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAAC  
ATTTCATCCTCCCGGGCGGCCCGCGCTGCGAGCGCCCCCGCCAGTCCGCGCCCGCCCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCGTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCTGCCACATTCCACGGCCTGGGCCCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCGTGAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCGCGCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCACTCTGGGCCTGGCTGCAGAAAGTTCCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTG  
ACAGCCCCGCCGGGCAACGGCTCTGGCCCACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCCTCCCTGATGGACGCGCTGCCGCCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA  
AAAA

**FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184  
><subunit 1 of 1, 473 aa, 1 stop  
><MW: 50708, pI: 9.28, NX(S/T): 6  
MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSEGGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

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**FIGURE 162**

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC  
AGTCCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAAACAATGGAGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTCTCTTTGGGCTTATCTCTGGCG  
GGCGCGCGGAACCTAGAAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTTAGGGTTG  
TTTCCAGAGGGGAACAAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACC CGCAAACGCGAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCCGTAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGCAGTCCGGTAGGCTTCTGGTTGTGAAGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACTAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTTCAGTGTTCAGATCTTGATTACGGAG  
AAAATGGGAAAATTAGTTGCTCCATTTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGGAGAGACCCTAGACAGAGAAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTTCGTC  
CGCGAGAACAACAGCCCCGCCCTGCACATCCGACGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCCAGGTCACCTACTCGCTGCTGCCGCCAGGACCCGACCTGCCCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGTCTCTGTTT  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCCGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCACTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

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**FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314  
<subunit 1 of 1, 798 aa, 1 stop  
<MW: 87552, pI: 4.84, NX(S/T): 5  
MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVS RGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLR FQVLLSPFEFFQAE LQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVD TG VNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAP EVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTL LTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELG LFGVWAH  
NGEVRTARLLSERDAAKHLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

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**FIGURE 164**

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

**FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 321-340

**Homologous region to dilsufide isomerase**

amino acids 212-302

**N-glycosylation site.**amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296**Thioredoxin domain**

amino acids 211-227

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**FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC  
TTTGGCCAGCCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCACTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTCCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCAACCGAATCTTGTAGAAATATTCAAACATAA  
AAATCATGAATATTTTAA

**FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920  
><subunit 1 of 1, 295 aa, 1 stop  
><MW: 33518, pI: 7.74, NX(S/T): 0  
MLQGPGLLLLLFLASHCCGLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSEKDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

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**FIGURE 168**

GTGGAGGCCGCCGACGATGGCGGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTG  
TATCCACCCCATTGCGGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTGCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCTTGTGGCCAATGTGCT  
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGAAGTGGACAGTGTCTCTGCTGCTGATGGCCG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCGGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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**FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988  
><subunit 1 of 1, 560 aa, 1 stop  
><MW: 58427, pI: 6.86, NX(S/T): 2  
MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQ RATANMLATMSNPLGVLVANVLSFVLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCFLSLACVPFALVSQ LQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAE GILIMLMTALT VRRSEPSLSTCQ QGEDPLDWTVSLLL MAGLCTFF  
SCILAVFFHTPYRRLQAESGEP PSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAA TDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

**Important features:****Potential Transmembrane domains:**

amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-  
268, 280-300, 318-337, 341-357, 375-387, 420-441

**N-glycosylation site.**

amino acids 40-43 and 43-46

**Glycosaminoglycan attachment site.**

amino acids 468-471

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**FIGURE 170A**

GTCCACATCCTGCTCAACTGGGTGAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCT  
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCCTTTGG  
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCTTGGGGTCTGCTTGTTCATAATCA  
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGGAAGGAGCACGGGGCTGATCAAGC  
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTTTTCTGAATCTA  
GCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG  
TGGCTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAG  
TGTCAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAG  
GAGAGGCGGAGGCAAGCTGGGGCCGCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT  
TCAGGTGGACTCTGAGGAAGGCTTGTGCTCAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT  
GCCGACAGTGGGATCCCTGCCTGGTTTTCTTTGATGTGCTTGCCACAGGGGATTTGGCTCTG  
ATCCATGTGGAGATCCAAGTGTGAGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCCGA  
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTC  
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTT  
GCCTTGGATGTCAATTGTGGGCCCTGATGAGACCAACATGCAGAACTCATAGTGGTGAAGGA  
GCTGGACAGGGAATCCATTTCATTTTGTATCTGGTGTAACTGCCTATGACAATGGGAACC  
CCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAGCCCT  
GCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT  
CATAAACTGACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCA  
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTC  
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTTCAGGCAAG  
GGACCTGGGTCCCAATCCTATCCCAGCCCAATTGCAAAGTTCTCATCAAGGTTCTGGATGTCA  
ATGACAACATCCCAAGCATCCACGTCAATGGGCCTCCCAGCCATCACTGGTGTGAGAAGCT  
CTTCCCAAGGACAGTTTTATTGCTCTTGTGTCATGGCAGATGACTTGGATTGAGACACAATGG  
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCA  
ACACATGATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCCAAATATACCCCTC  
ACTCTGTAGCCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTCA  
GATCAGTGACATCAACGACAATGCACCTGTGTTTTGAGAAAAGCAGGTATGAAGTCTCCACGC  
GGGAAAACAACCTTACCCTCTCTTCACTCATTACCATCAAGGCTCATGATGCAGACTTGGGC  
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA  
CTCCAACACAGGAGAGGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTTG  
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGATCCAGTGTCTCTGTGTGG  
GTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG  
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA  
CTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG  
CCATTCTTTGACAACCATTTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCTC  
CTACAGCATCCGCAATGGAAATGAAGCCCCACCTCTTCACTCTCAACCCCTCATACGGGGCAGC  
TGTTTCGTCAATGTACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA  
GTAGAGGACCAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTTGAGGGTTCATGTTTGTGAC  
CAGTGTGGACCACCTGAGGGACTCAGCCCCGAAGCCTGGGGCCTTGAGCATGTGATGCTGA  
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTCATGTCC  
ATCTGCCGGACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGCGGGAGGCCGAGTCCACCTA  
CCGCCAGCAGCCCAAGAGGCCCCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTG  
TGCTCAGGGGTGTCAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCACAAAGATGTGGACAAG  
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTCACCCTGAC  
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC  
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAAC  
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGC  
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC  
CAGCCTCCTCTGCAACCCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCCTGAGAAA  
GAATCAGGGCCCCGTCAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGCTGCCCTCGCCGA  
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAGCAAATCTCCAGCTGC  
TGTCCTTGCTGCATCAGGGCCAATTCCAGCCCCAAACCAACACCGAGGAAATAAGTACTTG  
GCCAAGCCAGGAGGCAGCAGGAGTGAATCCCAGACACAGATGGCCCAAGTGAAGGGCTGG

**FIGURE 170B**

AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA  
AGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCCACAGCAGGTCTGGCCCTGGAC  
CGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCCCTCACCACCAACTA  
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT  
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC  
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCGTGGAGGC  
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGAGGACCCTCAGTTTAGACTTGGCCA  
CCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC  
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCGTGTAACATACCTCAGACGCCTCTGGAT  
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCAC  
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAG  
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCTTGTAAGCAGCTCTGAGTCTTTTGG  
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAAACATATGTGGAGCACAAAG  
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT  
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGTGCCAGGAAATGCTCTCTGACCTATCAA  
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 171**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLGGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVDLATGDLALIHVEIQ
VLDINDHQPRFPKGEELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS
LALEIQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRS LNYEEMAGFEFQVIAEDSGQPMLASSVSVVWSLLDA
NDNAPEVVQPVLS DGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLQAPFHLTPTLTYRTLNRNQGNGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKPGGS
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATS AASGMKVQGDPPGKTGTGEGKSRGSS
SSSRCL
```

**Important features:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 172**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCACTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTCCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTCTC  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCCTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTGACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT  
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAATCACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATACCCGTTGGTT  
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAAGTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAATTTAGATATAAGAGGGGGGAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAAGTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGCGCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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**FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPFPLSPKHGILSIEQLISRVGIVGVITLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAISS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLWSA  
LSSILFLYLAHKQAPEKQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

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**FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTGGATTGGGTGGCTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

**FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTGAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTCTC

**FIGURE 176A**

CTCGCGCAGGGATCGTCCCATGCGCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGA  
TTTGCTACCTTTTTTGGCTCCCTGCTCGTCTGCTCGAACTGCTCTTCTCACGGGCTGTGCGCTTCAAT  
CTGGACGTGATGGGTGCCTTGCGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT  
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG  
CCCTGGCTCTTCTTGGGCAGCAGGCCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC  
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAG  
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGCCCTGGGGGCAAGATTGTTA  
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG  
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA  
ATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCA  
CAGCTGCCGCTTCTCCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT  
TGGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA  
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTG  
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAAGAGCTG  
AGCTTTGTGGCTGGAGCCCCCGCGCCAACCACAAGGGTGTGTGGTCATCTGCGCAAGGA  
CAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG  
GCTACTACTGGCTGTGGCTGACCTCAACAGTATGGCTGGCCAGACCTGATAGTGGGTGCC  
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGG  
GGGTCACTGGGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCTGGGA  
TCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC  
CCCTTTGATGGTGATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTTGTGCGCAA  
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTGAG  
GCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACC  
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG  
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG  
TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG  
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCTCTGAGCCG  
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCCTGTGGCTGAAGCACCAGCATGACC  
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGGCCATT  
GTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG  
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCACCAGCCCAGCAGCCAGCGGGCAGAGATCC  
ACTTCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC  
GCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACCTCTGCCCCATGGATGTGGATGG  
AACACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGATGGTCACCA  
ACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTC  
CTGGTCTATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAA  
GCCACTCTGCCTGTCCAATGAGAATGCCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGA  
AGAGAGGTGCCAGGTCACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTTGAGACC  
ACGGAAGTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC  
TGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTTCCCAGC  
AACTCTTCTTCTCTGGTGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC  
AGCAAGGTCAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCTGGGGCTC  
TGCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA  
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCC  
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGGAGCTGGAGCCACCTGA  
GCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGTG  
AGAAGAAGAAAAACATCACCTGGACTGCGGCCCGGGGACGGCCAACGTGTGGTGTTCAGC  
TGCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGCTCTCTGGAACAG  
CACCTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCA  
CAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATG  
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTCTCCTCTGGC  
TGTAAGTGGCTGGGCTGTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCT  
TCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGG  
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAAGTGGGGCAG

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**FIGURE 176B**

CCCCCGGCGGGAGGGCCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG  
GCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCCAGCCTGGCCTGTGG  
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG  
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGACAGACCTCTCCCACCCACAA  
GAACTCCTCCCACCCAACCTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC  
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT  
CCTAATCCCTTCCCTCTCCCATTCACCCTGTGTAACAGGACCCCAAGGACCTGCCTCCCCGGA  
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT  
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC  
TATTTATTAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGFACPLSLEETDCYRVDIDQADMOKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGWKFCFEG  
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVVYVLNQGQGHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGVAPFDGDGKVFYIYHGSSLGVVAKPSQVLE  
GEAVGIKSGFYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQPSSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALEFA  
LSGQPVIGLELMVTNLPSPDPAQPADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYILISTSGISIIETTELEVELLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGSRLTLGSAFLNIM  
WPHEIANGKWLLYPMQVELEGGQGPQKGLCSRPNIHLDDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLLWNSTFLEEY  
SAVKSLEIVIVRANITVKSSIKNLMRLDASTVIPVMVYLDPMVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPPREGP  
DAHPILAADGHPGLGPDGHPGPGTA

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1039-1064

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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**FIGURE 178**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGGCTCGAGACGGCGGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCTTTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTTCAGGGAAGTGGCAAACAGATTGCGGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGATACACAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

**FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREANRLRDWFKALHESGSQNKTKTLLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEDEGDDDDGGDDHDVYI

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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**FIGURE 180A**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA  
CAGTACCTGACGCCTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC  
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC  
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTTCCCGCCGGCCAGAAGGAGTGCTT  
CTACCAGCCCCATGCCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTGTAGTGGAGCAG  
GATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGA  
AAATCAGATGGAGTTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA  
TACATTCAGCACCATTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG  
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG  
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAAGTGGGCA  
CATACAAATTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG  
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAA  
GTTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACT  
AGAGTACGTAACATTGAAAAATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCAT  
TAATGGTCTTCTCCAAAATATTTTGTAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG  
AAAATTAAGTCTTCACTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAAGTGTGTA  
ACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC  
CTAACTTTGAAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAAT  
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAAGTCTTTTGTAAATGCGGCAGT  
TACAAATTAAGTGTGGAAGTTTTTCAAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA  
TGGATTGAATAAATCTTAGACTACAAAAGCCCAACTTTTCTCTATTTACATATGCATCTCT  
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGTAGATTTTTATAACC  
AAATACATTTCAAGTGAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC  
CAAAAGCTGACATTTTTCAGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACAT  
GTTTTCTCTTTGAAATGAAGAATATAGTTTTAAAGCTTCTCCTCCATAGGGACACATTTTC  
TCTAACCTTAACTAAAGTGTAGGATTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTT  
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAAC  
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG  
ATCTGGGCTTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG  
AAAGAATTTTGAATAAATCTGAGAAAACCTAATCCAAAATAAATTCACTTAAGTAGAAGTAT  
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAGG  
AGATGATTAATTTCCAGTTAGCTGGAAGAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA  
ATTCTGGTTTGAATTATTTTGTAAAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG  
GTTTAGCACTGGGTGTACATATTTATTAATAATTTTATTTATAACAACTTTTATTAATAATGG  
CCTTTCTGAACACTTTATTTATTTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT  
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGA  
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTT  
TTAAGTTATGCCATTTTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAACTTAAA  
ATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATCTTGATGAGCAATAATGA  
TAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA  
GGCCCTTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAATAAGGTTAA  
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAATGCTTCAGGTGTCTAGGGGTATCC  
TCTGCAACACTTGCAGAACAAAGGTCAATAAGATCCTTGCTATGAATACCCCTCCCTTTTG  
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG  
ATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTACCTCTCCTGTATGGC  
TGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC  
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTTACCATATAAAAAAC  
GATAATTGCTTTATTTGGAAAAGAAATTTAGGAATACTAAGGACAATTTATTTTATAGACAAA  
GTAAAAAGACAGATATTTAAGAGGCATAACCAAAAAGCAAACTTGTAACAGAGTAAAAA  
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTAATTTCACTAT  
TCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTTAACAGCTCATTT  
TGTCTTTTTCAATATACAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATT  
CCATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGTCTGTATGCA  
TTTGGATGATTAATGTTATGCTGTTCTTTTCATGTGAATGTCAAGACATGGAGGGTGTGTA

**FIGURE 180B**

ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAATGAG  
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA  
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACG  
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA  
ATAAAAATTATCAAAGGAAAA

**FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196  
><subunit 1 of 1, 229 aa, 1 stop  
><MW: 26017, pI: 4.73, NX(S/T): 0  
MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY  
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL  
ILDNMGEQAQE QEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 182**

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTTGATG  
CTGCTTTTCTGCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC  
TTCTTTTTCTTTTTCTTACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDFTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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**FIGURE 184**

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC  
TGCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

**FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVGIGQTLVPSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

**FIGURE 186**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC  
AATCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTTGAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

**FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQOTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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**FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGETCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

**FIGURE 189A**

GAGGAACCTACCGGTACCGGCCGCGCCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC  
CCGTGCGCCGCGGGCTGGGCGCTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGG  
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC  
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC  
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCTTGAAGTAATG  
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT  
CACTTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATA  
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC  
ACAGATCAGGATTTTACAGTTTACTTGGAGTGTCCAAACTGCAAGCAGTAGAGAAATAAG  
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG  
CACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG  
AAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG  
CTGGAACCTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG  
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAACTGTGGTTTGTAATTTTTACTCC  
CCAGGCTGTTTACACTGCCATGATTTAGCTCCCATGAGAGACTTTGCTAAAGAAGTGGGA  
TGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG  
GAGTCAACAGCTATCCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT  
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGAC  
AGAACTTTGGACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCT  
GGCTGATCACTTTTTGTTCAAAGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTT  
AGTGGCATGTTGTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA  
TCTTCCAGATTTTGAACACTTTTCGGCAAACACACTAGAGGATCGTTTGGCTCATCATCGGT  
GGCTGTTATTTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAACTA  
AAAACCTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCACCAGA  
CATCTGTAGTAATCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCA  
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAA  
AGTGTGAATTTCTCATGTTACCACGCTTGGACCTCAAAATTTTCTGCCAATGACAAAGAACC  
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACTACCAGAGTTAC  
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTAT  
GAGGGACTCTGTAAATGTATAACATTAGGCTTATCCAACAACAGTGGTATTCAACCAGTC  
CAACATTGATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATC  
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAAGTATTACACAAAGA  
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTATCCTTGCCAAGTCTT  
AATGCCAGAATGGAAAAGAATGGCCCCGACATTAAGTGGACTGATCAACGTGGGCAGTATAG  
ATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCTTGAGATAAGA  
TTTTTTCCCCCAAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA  
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACAC  
CTCAGACTTTTCACTGAAAAAGTTCTACAAGGGAAAAATCATTGGGTGATTGATTTCTATGCT  
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA  
AGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG  
GGATCAGGGCTATCCAACCTGTTAAGTTTTATTCTACGAAAGAGCAAAGAGAAATTTTCAA  
GAAGAGCAGATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTAAAAAATTGGA  
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTTTGAATAATGTTGAAGATGAAGAA  
AAAGTTTAAAGAAATTTCTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA  
TGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCAGAATTATCTACAGCA  
CTGGTGTAAGAAGGGTCTGCAAACCTTTTTCTGTAAAGGGCCGGTTTTATAAATATTTTGA  
CTTTGCAGGCTATAATATATGTTTACACATGAGAACAAGAATAGAGTCATCATGTTATCTT  
TGTTATTTGCTTTTAAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACA  
AAAGTAGGCTGGATTGAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG  
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT  
AAAGTCCACTTTCCCTTACGTTTTTTGGCTGACCTGAAAAGAGGTAAGTTAGTTTTTGGTC  
ACTTGTCTCTCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAAAACACCCA  
TGATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT  
TTCTTTCTTCTCAAAGGTTGAAAAAATGCTTTTAATTTTTTACAGCCGAGAAACAGTGCAG

**FIGURE 189B**

CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG  
TTTGCTGTATCATCCAGGAAAACCTGAGGGAAAAAAATTATAGCAATTAAGTGGGCATTGTA  
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTTCA  
GTATTTTCTGAAATTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTGGAGGCATCTA  
ATATTTACATATTTGCCTTCTGAACCTTGTGTTTGACCTGTATCCTTTATTACATTGGGTTT  
TTCTTTTATAGTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT  
TACTTTACAGGTTGTTTTTACTGTAGCTTATAATGATACTGTAGTTATTCCAGTTACTAGTTT  
ACTGTCAGAGGGCTGCCTTTTTTTCAGATAAAATATTGACATAATAACTGAAGTTATTTTTATAA  
GAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAAA  
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTGAGAGTGTACAGAATGGT  
AAAAATTCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTTCAAAAAAA  
AAAAA



**FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439  
<subunit 1 of 1, 747 aa, 1 stop  
<MW: 86127, pI: 7.46, NX(S/T): 2  
MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFCCKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSPLYVFQP  
SLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVS LTPPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTD LTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQKRNKDEL

**Important features:**

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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**FIGURE 191**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTACAGAGGTCTGACATCAGAACCTCAGGCCTT  
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTT  
TCAGTCTGTATAATATTA AAAACATTGGTTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGACCCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTAAATCTCAGAATTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

**FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409  
<subunit 1 of 1, 300 aa, 1 stop  
<MW: 33655, pI: 9.31, NX(S/T): 1  
MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCNREEIYRSLNQVKKEVGDVTIVVNNAGTV  
YPADLLSTKDEEITKTFFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFGHRLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPFVLETDEVVRSRID  
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.  
amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein  
amino acids 165-202, 37-49, 112-122 and 210-219

**FIGURE 193**

CGGCGGGCGGCTGCGGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCCGCGGGG  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT  
GCTGATCATCGTGACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCAG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

**FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSVMILLIIVYWD SAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELT  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFTP KERA FDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWK RVMIVLS  
GSELLHRGAPYRDPLRIPREHVHNASAH LTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAQAQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLF GYPK PENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

**FIGURE 195**

TCGGGCCAGAATTCCGGCACGAGGCGGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCSCCGATTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGGGGCTGCGGCAGTGTTCTTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTCTCTCATTT  
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

**FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045  
<subunit 1 of 1, 270 aa, 1 stop  
<MW: 28317, pI: 6.00, NX(S/T): 1  
MATGTRYAGKVVVVTGGGRGIGAGIVRAFNNGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLLDCVNNAGHHPPQRPPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVLGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

**FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG



**FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSPRIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIavgctcIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

**FIGURE 199**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCGGAGAAGCCTCGCTCG  
GCGCCCAACATGCGCGGGTGGGCGCTGCGGCCCCGAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCGCGCTGCCGCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTCTCCCAGCATTTTTTCATGCAAAGGATGGGATATTCGCCGT  
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACCTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGGACGGTGTC  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGC  
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTAAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTTCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCACTCTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAATATAGTTGTTGTTGATTTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAA  
GAATTAATGAATCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTCTGTATC  
TTCCAAAGAATTATATCTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

**FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433  
<subunit 1 of 1, 349 aa, 1 stop  
<MW: 38952, pI: 4.34, NX(S/T): 1  
MAGGRCGPQLTALLAAWIAAVAATAGPEEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSQCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

**FIGURE 201**

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCACATGATT  
TGA CTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC  
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCTTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATGTAAGAGGAAGGTTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGTATCTCTCGC  
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTA  
CTTTTTCTTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTGCGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTTCACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA  
TTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCA  
TTCAATAAAAAAAACTCTTATCAAAAAA

**FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

**Important features:**

**Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

**FIGURE 203A**

GGAAGGGGAGGAGCAGGCCACACAGGCCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG  
TCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC  
TCCCCGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAC  
TTCCAAGAGTGA CTCCGTGCGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT  
CCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGGGAAGACTTTTC  
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC  
CTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTTCCTGCAGC  
CCACCCTGCTTCCCGATCCTTCCCTGACCCAGGGGCCTCTACCACTTCTGCCTCTACTGGA  
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA  
GCCTCTAGCCTCCTCTGCTTCCAGCACCCAGGAGGAGAGCCTGGCTCAGGGCCCCCGCTGTT  
AGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCCAGTGCCGCCAGCT  
TCACCTTCTCCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC  
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAG  
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGGTGCAGAGCCTGGAGTCGAAACTGACCTCTG  
TGAGATTCTGAGGGGACATGGTGTCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG  
CTCCAGCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG  
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGAGGAGGAGCCGGA  
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC  
AAGAATTCAGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT  
AGCCAACCTCACGGAGCCCGTGGTGTCTACTTTCCAGCACCAGCTACAGCCGAAGAATGTGA  
CTCTGCAATGTGTGTTCTGGGTTGAAGACCCACATGAGCAGCCCGGGGCATTGGAGCAGT  
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA  
CTTTGCACTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTCACAAGCACTACCTGAGCC  
TCCTCTCCTACGTGGGCTGTGTCTCTGCCCCTGGCCTGCCTTGTACCACTTGCCGCCTAC  
CTCTGCTCCAGGTGCCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA  
CATGAACCTGCTGCTGGCCGTCTTCTCTGCTGAGACACGAGCTTCTGCTCAGCGAGCCGGTGG  
CCCTGCAGGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCTGCACCTTCTCCCTGCTC  
ACCTGCCTTTCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT  
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT  
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTG  
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG  
CTACATCACCAACCTGGGCCTCTTTCAGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCA  
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCACACCCAAAAGTGGTCACATGTGCTGACA  
CTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTC  
TGGCACCTTCCAGCTTGTGCTCCTTACCTTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC  
TCATCTTCTATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCTCTGAAG  
AGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA  
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT  
GGCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC  
ATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT  
GGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA  
GGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG  
GGCCAGCCCTCATTTGCTGGGGGCCAGGCCTTGGATCTTGGAGGTCTGGCACATCCTTAATC  
CTGTGCCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCTGA  
GGGCACTCTGCATCCTCTGTCTATTTTAACTCAGGTGGCACCCAGGGCGAATGGGGCCCAGG  
GCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGCAG  
CTCGCTACCTCTGAGCCCAGGCCCTCCCTCCCTCAGCCCCCAGTCTCCCTCCATCTT  
CCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCC  
GATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT  
TTGTCTACTGCACAAGCCTCGGCCCTGCCCTGAGCCAGGCTCGGTACCGATGCTGCTGGGCTGG  
GCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGTCTACCTTGACC  
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAAGTGTGG  
ACCATGCCAGTCCCGTCTGGTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTG  
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTC

**FIGURE 203B**

CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTAGATTGC  
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC  
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAAGTCTCTGGAGCTACAGGGACAGGGAGCCAT  
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA  
AGATGGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA  
CATGTTCAATTGTAGAGAATTTGGAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAG  
CTGTTGTAATCGCCTAGCAA  
AAA

**FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921  
<subunit 1 of 1, 693 aa, 1 stop  
<MW: 77738, pI: 8.87, NX(S/T): 7  
MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPT?DLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVD FSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGC VVSALACLVTIAAYLCSRVP LPC  
RRKPRDYTIKVH MNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

211/237



**FIGURE 205**

TGCCTGGCCTGCCTTGTCACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACCTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTTCTGTTCAACATGG

**FIGURE 206**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA  
GGTTTTGCTTTGATCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT  
GGATGGGATTATGTGGAACTACCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC  
ACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT  
GCCCCCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCT  
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT  
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT  
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATAC  
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCTACGTTTGATG  
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG  
GAACCCAGTGTATGGAATATATTAGGGCGCTGGTGTGGTCTGCTACTGTACCAGGAAAACA  
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAAC  
CAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCA  
GTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC  
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT  
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTCTTGGGAAGAAAATCCAGAGTGGTG  
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGT  
GTCCATAAGGGAAGAACTAAAGAGAACCAGTATACCATTTTCTGGCCAGGTTGTCTCCTGGTTA  
AACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA  
AGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGG  
ATTGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA  
GAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGC  
AGTGGCTGATTCATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT  
CAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT  
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC  
GTGGAAAGAAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTA  
CGTATTTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGT  
ACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGGTTGCCCTTGCTTAACCTAAAGCTCC  
ATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCAC  
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCT  
ATGAATTAACTTGTGTCTGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATAAT  
TTCTGCCATTTAGAAGAAGAGAACTACATTTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAG  
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTAT  
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTAC  
CAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATT  
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC  
AAAAATACATGTATTTCACTCTCGTATGGTCTAGAGTTAGATTAATCTGCATTTTAAAAAA  
CTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTGGAAAATAATTAAATTATCATATC  
TTCCATTCTGTATTATTGGAGATGAAAATAAAAAAGCAACTTATGAAAGTAGACATTCAGATCC  
AGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGC  
ACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT  
CCTATTTATTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAAT  
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCA  
ATTTAAAAGAAAATCAGTAAAATATTTTGCTTGTAATAATGCTTAATATNGTGCCTAGGTTAT  
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAAGAATGTGGCTATTTTGG  
GGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

FIGURE 207

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCRCGSTGG

**FIGURE 208**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT  
CCATTTTGAAGAAGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCTTA  
TCCTTTTTTAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTG  
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA  
TTTGACAGAAATTCTGGAGGTATTCCCACGAACACCACGAACCTCACCTCACCATTAACC  
ACATACCAGACATCTCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTC  
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA  
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACC  
AGCTACTAGAGATACCGCAGGGCCTCCCGCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC  
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT  
GGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT  
TCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAAGATAACAATGTACAGCCGTCCTT  
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA  
AGAAGATGATTTTAATAACCTCAACCAATTACAAATCTTGACCTAAGTGGAAATTGCCCTC  
GTTGTTATAATGCCCATTTCTTGTGCGCGTGTAATAAATCTCTCCCTACAGATCCCT  
GTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTACGTCTACACAGAACTCTCTTCA  
GCATGTGCCCCCAAGATGGTTAAGAACATCAACAAACTCCAGGAAGTGTCTGTCCCAA  
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAA  
TTGGATCTGTCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAGC  
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA  
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT  
AAGCTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA  
TCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAATG  
CCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAATTACATTATTTTCAGATAT  
GATAAGTATGCAAGGAGTTGCAGATTCAAAACAAAGAGGCTTCTTTCATGTCTGTAAATGA  
AAGCTGCTAAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT  
CCTCTGATTTTCAGCATCTTTCTTCCCTCAAATGCCTGAATCTGTGAGGAAATCTCATTAGC  
CAAACCTCTTAATGGCAGTGAATTTCCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA  
CAACCGGCTTGATTTACTCCATTCAACAGCATTGGAAGAGCTTCACAACTGGAAGTTCTGG  
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC  
AAGAACCTAAAGGTTCTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAG  
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT  
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA  
TTAGACATCTCTAAAAATTCCTTAAGTTTCTTGCCCTTCTGGAGTTTTTGTGGTATGCCTCC  
AAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAACTTTTCAGTTGGAAGAACTCC  
AGTGTCTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG  
AGATTATCCAACCTGTTCCAGAAGCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG  
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA  
AAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTCAACAATCTGAAGATGTTG  
CTTTTGATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGGTTAA  
CCATACGGAGGTGACTATTCCCTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC  
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG  
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCA  
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC  
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATGTGTATGACACTAAAGACCCA  
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAAACTGGAAGACCCAAGAGAGAAACA  
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT  
CCCAGAGCATAACAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACT  
GAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGT  
GATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAGAGTCCAAGTTCTCCAGCTCCGGAAAA  
GGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAAACCCGCAAGCTCACCCATACTTCTGG  
CAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATAGTCAGGTGTTCAAGGA  
AACGGTCTAGCCCTTCTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

**FIGURE 209**

MVFPMWTLKRQILILFNIIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRDLHVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYRR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TDLDSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL  
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHNRFLCTCDVWVFWVWNHTEVTIP  
YLATDVTGCVGPAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLLE  
RDWLPGQPVLLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**FIGURE 210A**

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA  
AACATGTTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGA  
GTTATGCGCCGAAGAAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACT  
CAGTTATTGCAGAGTGCAGCAATCGTCTGACTACAGGAAGTTCCCCAAACGGTGGGCAAATAT  
GTGACAGAAGTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAATCATTTTCAAGG  
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA  
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAAC  
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGGCAGAGTC  
TTTGACAGAAGCTTAGTCTAATTTCAAACAATATATACAACATAACTAAAGAGGGCATTTCAA  
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTGTATTTTAACAAAGTTTGGCGAG  
AAAATAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC  
TTTCAATTCTCTTTTACACGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCTGA  
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTCAAGGGATTGATAAATTTAACATTA  
CTAGATTTAAGCGGGAACTGTCCGAGGTGCTTCAATGCCCATTTCCATGCGTGCCTTGTGA  
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAACTTGACCCAACTTCGATACC  
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTTAAAAATATGCCTCAT  
CTGAAGGTGCTGGATCTTGAATTCACATTTTAGTGGGAGAAATAGTCTCTGGGGCATTTTTT  
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC  
CACAGCATATTAATATTTCCAGAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTA  
AGAGGTTATGTGTTCCAGGAAGTCAAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA  
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACCTTTTCCAAA  
ATTTCTCCAATCTGGAAATTAATTTACTTGTGAGAAAACAGAATATCACCGTTGGTAAAAGAT  
ACCCGGCAGAGTTATGCAAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC  
AGATTTTGAGTTTGACCCACATTCGAACCTTTTATCATTTACCCGTCCTTTAATAAAGCCAC  
AATGTGCTGCTTATGGAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA  
AACCAATTTGAAAATCTTCTGACATTGCCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCA  
AGTGTTAAGTGGAACTGAATTTTCAGCCATTCTCATGTCAAATATTTGGATTTGACAAACA  
ATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT  
CTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA  
AAATTTACAAATCTAAAAGTTTAAACTTGAGCCACAACAACATTTATACTTTAACAGATA  
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATT  
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG  
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCTTAATTTGCCAG  
CGAGTCTCACTGAAGTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC  
CAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTTAACTGA  
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC  
ACCTACCCTCTGGCTTTCTTTCTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT  
CTGCTAAAAACAATCAACAAATCCGCACTTGAAACTAAGACCACCACCAATTTATCTATGTT  
GGAAGTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG  
ATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCTGGGGAT  
CAAAGAGGGGAAGAGTATTGTGAGTCTGGAGCTAACAACCTTGTGTTTCAGATGTCAGTGCAGT  
GATATTATTTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACC  
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC  
AGGTCTCTTTCCACATCCCAAACCTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC  
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTGAAGAGAGCCGAGACAAAA  
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC  
ATGCAGAGCATCAACCAAGCAAGAAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG  
CTGGAACCTTTAAAACAGCTTTTTACTTGGCTTTGTCAGAGGCTAATGGATGAGAACATGGATG  
TGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAG  
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG  
GCAAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTGCG  
ATTCCATTAAAGCAATACTAACTGACGTTAAGTCATGATTTGCGGCCATAATAAAGATGCAAA  
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATATCCCAAACCTTAGTGG  
TTTAAAACAACACATTTGCTGGCCCAAGTTTTTGGAGGTGAGGAGTCCAGGCCCAGCATAA

**FIGURE 210B**

CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTACCAGAGACATAGGC  
ATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA  
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCACAAGGCAGCTTGCTTCATCAGAGCT  
AGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAG  
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT  
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT  
TGCTTCAGTTGGTCATCACTATTTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG  
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA  
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC  
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCG  
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATG  
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA  
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA  
AATGAATGAATAAAAAATGTTTCATTTTACAAAAAAAAAAAAAAAAAAAA

**FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQND SVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELS LIQNNIYNITKEGISRLINLKNLYLAWNCYFNKY  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNL TQLRYLNLSSSTSLRKINAAWFKNM  
PHLKVLDLEFN YLVGEIVSGAFLTMLPRLEILDLSFN YIKGSYPQHINISRNF SKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNF SNLEIIYLS ENRISPLV  
KDTRQSYANSSSFQRHIRKRSTD FEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV  
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTE LHINDNMLKFENWT  
LLQQFPRELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHL DLS  
SNLLKTINKSALETKTTTKLSMLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQT FYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAIID  
NMQSINQSKKT VFLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY



**FIGURE 212**

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTGGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCCTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTACGCGGCCCTGCAGCCCCCATGCCCCCTGCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAATGAAACGTGA  
AAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTTTATTGCAGCTTATAATGGTTACAAAT

**FIGURE 213**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadgtLCVpKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

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**FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**FIGURE 216**

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCGCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGAGGAGCAGCT  
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTG

**FIGURE 217**

M R G S Q E V L L M W L L V L A V G G T E H A Y R P G R R V C A V R A H G D P V S E S F V Q R V Y Q P F L T T C D G H R A C  
S T Y R T I Y R T A Y R R S P G L A P A R P R Y A C C P G W K R T S G L P G A C G A A I C Q P P C R N G G S C V Q P G R C R  
C P A G W R G D T C Q S D V D E C S A R R G G C P Q R C V N T A G S Y W C Q C W E G H S L S A D G T L C V P K G G P P R V A  
P N F T G V D S A M K E E V Q R L Q S R V D L L E E K L Q L V L A P L H S L A S Q A L E H G L P D P G S L L V H S F Q Q L G  
R I D S L S E Q I S F L E E Q L G S C S C K K D S

**FIGURE 218**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCAGGAGGAGACAGCCTC  
CCGGCCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTC  
CGTTTCCTGCCGTCAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC  
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTCCAGGGCTAGCAA  
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG  
GGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAACCCATTTTGGAGCAGGAATTCCAA  
TCATGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCCAGGCAGG  
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCCGGCAAAGGGCATTTTCTACCTGAC  
CCTTTTCCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG  
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCTTTTCTCCATGGCTACA  
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATGAAGCAGC  
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC  
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC  
AAGACTTTCGGCCCTCCCCGGGCCCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTT  
CGACCATCACTGCCCCCTGGGTGGGGAATTGTGTGGAAAGAGGAACTACCGCTACTTCTACC  
TCTTCATCCTTTCTCTCTCCCTCCTCACAATCATATGTCTTCGCCTTCAACATCGTCTATGTG  
GCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTTGAAAGAACTCTGGAACCTGTTCT  
AGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCTACTT  
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAAT  
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG  
CCCCTTGCCCCCAGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC  
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCCACAGAA  
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA  
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT  
TTTGTGTTGTGTTAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAG  
AGCAATAAGCTGTCCCTTTTAACTGTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG  
GCATTTTCTTGCTGCAAGCTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAGATGTCAG  
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA  
GCCACAGGGTCCCCTTGGAACCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTC  
ACTGGTCTCATTTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA  
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGG  
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC  
AGCATTGCCCCACAAATCCTTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTANNNNNNN  
NNNNNNNNNNNNNNNNNNNTTGTTTTCTTTTGAAGTCTGCTCCCATAGGAGCAGGAATG  
GCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCCGAGTGCTCACT  
TAAACACTATCCCCCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG  
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAA  
AAAAATGCTAACCAAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAGCCCAGCACTGCTG  
CCCTCTCGGGTAACTCACCTAAGGCTCGGCCACCTCTGGCTATGGTAACCACACTGGGG  
GCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCAACC  
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAGGGAAGAAG  
ATTTATGTATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAG  
GGTCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAACCGGAACTTTTCTATTTGAA  
GGCGATTAACTGTGTCTAATGCA

**FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFECRYLAV.  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGNRYRYFYL  
FILSLSLTLTYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVGLTGFTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PFSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEA EK



**FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

**FIGURE 221**

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTCT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACCTCATCTTCTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAAGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGAACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

**FIGURE 222**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNR  
VTRVAWLN RSTILYAGNDKWCLDPRV VLLSNTQTQYSIEIQNV DVYDEGFPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYEC SASNDVAAPV VRRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV  
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLI FFNVSEHDYGN YTCVASNKLGH TNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

**FIGURE 223**

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

**FIGURE 224**

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGGGCCGGGAGCGGGCCAGCTG  
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGG  
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG  
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT  
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACAGAGGCCTGCA  
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTT  
TACCAGTTCTCTGTGGGGGCTGGATTGCGAGGAACCCCTGCCCGATGGGCGTTCTCGCTG  
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA  
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA  
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGAGACCTCATTGAGAAGATTGG  
TGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAAGGCAGTAG  
CAGGGACCTACAGGGCCACCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCC  
AACAGCAATGTTATCCAGGTGGACAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT  
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGA  
TGCTGCTGGGTGGGCGGGCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGGA  
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCAGCAGGAGAAGATCTACCA  
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCTGT  
CTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT  
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT  
GATCTGGAACCTGGTGCAAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG  
AGAAGCTGCTGGAGACCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC  
ATCTCCAACACGGATGACGCCCTTGCTTTGGGTCCTTTGCGTGAAGGCCACGTT  
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAGG  
AGGCCCTGGGACAGCTGGTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA  
GATGCCATCTATGATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA  
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAACATGTTGAATTTGTACA  
ACTTCTCTGCCAAGGTTATGGCTGACCAGTCCGCAAGCCTCCAGCCGAGACCAGTGGAGC  
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGC  
TGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCA  
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC  
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACAC  
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC  
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA  
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCA  
GCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACG  
AGGGGCTGGTGACCGACCCCCACAGCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAAC  
TCCCGTGACTTCTGCGGCACCTTCGGCTGCCCTGTGCGCTCCCCATGAACCCAGGGCAGCT  
GTGTGAGGTGTGGTTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCA  
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT  
CTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCTCCTCAATCACCACATTGTGCCT  
CTGCTTTGGGGGTGCCCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGT  
GTCACCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

**FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQQA  
ILKHLLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTYYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

**FIGURE 226A**

GCCCCGGCCCTCCGCCCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCCGCTCCCGCGCCCTCCTC  
CCTCCCTCCTCCCCAGCTGTCCCGTTCCGCTCATGCCGAGCCTCCCGGCCCGCCGCGCCCCG  
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGCGCCCGCGCGCCCGCCAGAGCC  
CCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCCGGGGAGCGGCAGGTAGGT  
GGGCGCCCCGGGGAGGCGCGGGCGGGGAGTCGGGCTCGGGGCGAGTCAGCGCCAGCCCGGAG  
GGGGCGCGGGGCGCAGGTGGCTCGGCGCGGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAG  
GGCGCGGTGCCTGGGACCCGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTG  
GGCAGCGGCCTCCAGCCAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCC  
TTGGACGAGACGTGGCACCCGGACCTAGGGGAGCCATTCCGGGGTGATGCGCTGCGTGCTGTG  
CGCCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA  
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC  
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCAG  
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCTGGACC  
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTGAGCACCCTGCAGCC  
CCCACCCAAGATGGCCTGCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCT  
CCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCACCCTTCAGGGGAGGTCT  
GGGGGCCTCTCATCCGGCACCCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGACTCTA  
GAAGGCCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGA  
CTCCTTGCAATTTTTTGCTGCTCTTCCGAGGCCTTGCAGGACTAACCAGGTTCCCTTGAGGC  
TCCAGATTCTACACCAGGGGCGAGCTACTGCGAGAATTCAGGCCAATGTCTCAGCCCAGGAA  
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG  
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG  
CTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCCA  
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCT  
CCAGGTGCAATTGGTAGGGACAACCAAGTGAAGTGGTGGCCATGACACTGGAAACCAAGCCTC  
AGCGGAGGGATCAGCCCACTGTCTGTGCCACATGGCTGGCCTATCCTCCCTGCCCCAGG  
CCGTGGGTATCTGCCCTGGGCTGGGGTGGCCGAGGGGCTCATATGCTGCTGCAGAATGAGCT  
CTTCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC  
CTGCCCTACTGTGGGGCATAAGCGCCCGCCCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTA  
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCTTGGATACCCACTGTCACT  
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCACC  
TCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG  
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAGGCATGGC  
TTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC  
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGGCGGGCCGAG  
GGGGTGCGGGGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGGCTGTCT  
CCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTTGGGCGGGCCCCGAGACCCCAACATGCT  
TCTTCGAGGGGCGAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGC  
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCCGCCAG  
CTGCCACACCCGGTGCAGGCTCCCGACCAGTGTGCCCTGTTTGGCCTGGCTGCTATTTTG  
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGC  
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA  
GGTGCAGTGTCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCA  
AACAGTGTCCAGGTGAGGCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGG  
GGCTGCCGTTTTGCTGGGCAGTGGTTCAGAGAGTCAGAGCTGGCACCCTCAGTGCCCCC  
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT  
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAGAA  
GCTGAAGGTCACTGTGTCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTGTCTTGTACC  
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGG  
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCACCGGCGGCGTAAGTGAGGGAGTCCAGG  
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC  
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGC  
AACCTGGTGGAAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA  
AATTAAGCAACGAGATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC

**FIGURE 226B**

CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC  
TCCCTCTCCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT  
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA  
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCAATTCTCCTGTGG  
GAAGCCCAAGTGCCCTTTGCTCCTCTGTCTGCTCTACTCCCACCCCCACTACCTCTGGGAAC  
CACAGCTCCACAAGGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT  
GCCCTGCCACCCTCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTTCTGTACATAATGTCA  
CTGGCTTGTTGGGATTTTAAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC  
CTGCTGCCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTGTATTTATTAAACATTTCT  
TTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG  
AGAAGGGGCGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA  
CCTGGAGAGGCAGAGGATAGCGTGGCNNTTGGCTGGCATNCCTGGGTTCCGCAGAGGGGCTG  
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAGTAGAAGCAGGATTTTGA  
CTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGTCTGACTTCATGTTTGAAGTTGCTCCAG  
AGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTTC  
CCTCCCCCTCCCCTCCCCTCCCCTCCCCTCC



**FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGGCGGCCGTGATGGCTGGTGACGGCGGGGCGGGCAGGGGA  
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCTGGCCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCCGA  
GGAACCCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCA  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCCTTCCTTCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCC  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

**FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAAC TCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCCGTGTGCTCCTTGTGCCACTGCTCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC